GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:50:08 ; Search time 2.73403 Seconds
(without alignments)
203.984 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....DELVARFLPMLKLLTFDQQI 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	9.0	421	1	US-10-858-730-2	Sequence 2, Appli
2	75.5	8.1	522	1	US-10-793-626-456	Sequence 456, App
3	75.5	8.1	522	1	US-10-793-626-2042	Sequence 2042, Ap
4	75.5	8.1	724	1	US-10-793-626-968	Sequence 968, App
5	75	8.0	655	7	US-11-045-802-29	Sequence 29, Appl
6	74	7.9	581	7	US-11-045-802-30	Sequence 30, Appl
7	74	7.9	584	7	US-11-045-802-31	Sequence 31, Appl
8	73	7.8	579	7	US-11-045-802-32	Sequence 32, Appl
9	72.5	7.8	610	1	US-10-858-730-292	Sequence 292, App
10	72	7.7	579	7	US-11-045-802-33	Sequence 33, Appl
11	71	7.6	1192	1	US-10-858-730-72	Sequence 72, Appl
12	70.5	7.6	530	1	US-10-858-730-67	Sequence 67, Appl
13	70.5	7.6	597	7	US-11-045-802-28	Sequence 28, Appl
14	70.5	7.6	692	7	US-11-045-802-26	Sequence 26, Appl
15	69.5	7.4	360	7	US-11-082-389-90	Sequence 90, Appl
16	69.5	7.4	360	7	US-11-082-389-92	Sequence 92, Appl
17	69.5	7.4	719	1	US-10-793-626-1548	Sequence 1548, Ap
18	68.5	7.3	516	7	US-11-045-802-36	Sequence 36, Appl
19	68.5	7.3	565	7	US-11-045-802-34	Sequence 34, Appl
20	68.5	7.3	710	7	US-11-045-802-2	Sequence 2, Appli
21	68.5	7.3	710	7	US-11-045-802-19	Sequence 19, Appl
22	68.5	7.3	710	7	US-11-045-802-20	Sequence 20, Appl
23	68.5	7.3	710	7	US-11-045-802-21	Sequence 21, Appl
24	68.5	7.3	710	7	US-11-045-802-22	Sequence 22, Appl
25	68.5	7.3	710	7	US-11-045-802-23	Sequence 23, Appl
26	68.5	7.3	710	7	US-11-045-802-24	Sequence 24, Appl
27	67.5	7.2	611	7	US-11-082-389-436	Sequence 436, App
28	67	7.2	602	1	US-10-793-626-2362	Sequence 2362, Ap
29	67	7.2	828	1	US-10-467-962B-99	Sequence 99, Appl
30	66.5	7.1	364	1	US-10-984-376-5	Sequence 5, Appli
31	66.5	7.1	364	1	US-10-984-376-6	Sequence 6, Appli
32	66.5	7.1	540	7	US-11-045-802-35	Sequence 35, Appl
33	66.5	7.1	598	7	US-11-082-389-398	Sequence 398, App
34	66.5	7.1	911	1	US-10-858-730-9	Sequence 9, Appli
35	66	7.1	403	1	US-10-858-730-27	Sequence 27, Appl
36	65.5	7.0	246	1	US-10-793-626-2166	Sequence 2166, Ap
37	65.5	7.0	1451	7	US-11-046-346-1	Sequence 1, Appli
38	65	7.0	488	1	US-10-485-517-307	Sequence 307, App
39	64	6.9	1992	7	US-11-013-759-3	Sequence 3, Appli
40	64	6.9	1992	7	US-11-013-759-13	Sequence 13, Appl
41	64	6.9	2047	7	US-11-013-759-4	Sequence 4, Appli
42	64	6.9	2047	7	US-11-013-759-7	Sequence 7, Appli
43	63.5	6.8	782	1	US-10-793-626-2352	Sequence 2352, Ap
44	63	6.8	403	1	US-10-858-730-28	Sequence 28, Appl
45	63	6.8	418	1	US-10-858-730-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-858-730-2
; Sequence 2, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Amycolatopsis mediterranei
US-10-858-730-2

Query Match 9.0%; Score 84; DB 1; Length 421;
Best Local Similarity 27.1%; Pred. No. 0.39;
Matches 42; Conservative 23; Mismatches 64; Indels 26; Gaps 8;

```
Qy          2 SNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATA 61
              |:   | ||  :        ||   :  | :|   ::: ||: | | ||      :|   |
Db        234 SDKPGTTVTGSIEEIPVEQALITGVAHDRSEA--KITVTGVPDHTGAAAR----IFRVIA 287

Qy         62 DALVTDFYDHLESYE-----RTQDLF----ANSTKTVEQLKETQAEYLLGLGRGEYDTEY 112
              || : |    |::        ||   |    ||  | |::|:: |||  :|     ||
Db        288 DAEI-DIDMVLQNVSSTVSGRTDITFTLSKANGAKAVKELEKVQAE--IGFESVLYDD-- 342

Qy        113 AAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDA 147
                :||:  |:| |   : |    :   | :|
Db        343 -----HVGKV-SVVGAGMRSHPGVTATFCEALAEA 371
```

```
RESULT 2
US-10-793-626-456
; Sequence 456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 456
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-456

  Query Match             8.1%;  Score 75.5;  DB 1;  Length 522;
  Best Local Similarity   23.2%;  Pred. No. 3;
  Matches   49;  Conservative   30;  Mismatches   87;  Indels   45;  Gaps    9;

Qy          4 DNDTLVTAD--VRN----GIDGHALADRIGLDEAEIAWRLSFTGIDD------------ 44
              || :|:  |  |:|     | |:    |  ::||:    :: :|::|
Db        145 DNVSLIKLDGTVKNFRVTKIFGYFGLKREEIEEAQAGDLIAVSGMEDINVGETVTPHDHR 204

Qy         45 DTMAALAAEQPLFEATADALVTDFYDHLESY---ERTQDLFANSTKTVEQLKET---QAE 98
               | :  |  ::|  | |     : |      |    : |:      :|   || |   | :
Db        205 DPLPVLRIDEPTLEMTFKVNNSPFAGREGDYVTARQIQERLDQQLETDVSLKVTPTDQPD 264

Qy         99 YLLGLGRGEYDTEYAAQRAR-------IGKIHDVLGLGPDVYLGAYTRYYTGLLDALADD 151
                :  ||||       :  |       : |        | | |    |   |:|    :
Db        265 SWVVAGRGELHLSILIENMRREGFELQVSK--------PQVIL----REIDGVLSEPFER 312

Qy        152 VVAD-RGEEAAAAVDELVARFLPMLKLLTFD 181
              |  :   | | | :: | ||   || ::| |
Db        313 VQCEVPSENAGAVIESLGARKGEMLDMMTTD 343


RESULT 3
US-10-793-626-2042
; Sequence 2042, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2042
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-2042

  Query Match             8.1%;  Score 75.5;  DB 1;  Length 522;
  Best Local Similarity   23.2%;  Pred. No. 3;
  Matches   49;  Conservative   30;  Mismatches   87;  Indels   45;  Gaps    9;

Qy          4 DNDTLVTAD--VRN----GIDGHALADRIGLDEAEIAWRLSFTGIDD------------ 44
              || :|:  |  |:|     | |:    |  ::||:    :: :|::|
Db        145 DNVSLIKLDGTVKNFRVTKIFGYFGLKREEIEEAQAGDLIAVSGMEDINVGETVTPHDHR 204

Qy         45 DTMAALAAEQPLFEATADALVTDFYDHLESY---ERTQDLFANSTKTVEQLKET---QAE 98
               | :  |  ::|  | |     : |      |    : |:      :|   || |   | :
Db        205 DPLPVLRIDEPTLEMTFKVNNSPFAGREGDYVTARQIQERLDQQLETDVSLKVTPTDQPD 264

Qy         99 YLLGLGRGEYDTEYAAQRAR-------IGKIHDVLGLGPDVYLGAYTRYYTGLLDALADD 151
                :  ||||       :  |       : |        | | |    |   |:|    :
Db        265 SWVVAGRGELHLSILIENMRREGFELQVSK--------PQVIL----REIDGVLSEPFER 312

Qy        152 VVAD-RGEEAAAAVDELVARFLPMLKLLTFD 181
              |  :   | | | :: | ||   || ::| |
Db        313 VQCEVPSENAGAVIESLGARKGEMLDMMTTD 343


RESULT 4
US-10-793-626-968
; Sequence 968, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 968
;   LENGTH: 724
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-968

  Query Match             8.1%;  Score 75.5;  DB 1;  Length 724;
  Best Local Similarity   23.1%;  Pred. No. 4.5;
  Matches   48;  Conservative   28;  Mismatches   75;  Indels   57;  Gaps   11;

Qy          4 DNDTLVTADVRNGIDGHALADRIGLDE--AEIAWRLSFTGIDDDTMAALAAEQPLFEATA 61
              |||      |: | |  | ||:   :|:  ||  :   : |    | :  :
Db        111 DNDVDKEQDIINKI-VHILANEAIIDKKIAEDQYMYDYYGELKDELNYI---------- 158

Qy         62 DALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEY-DTEYAAQRAR-- 118
                  |:|:|     :|: :|     :    ||   |||:|  :| ||    ::
Db        159 -------YNHIEERLTLKDI-SNKLYVSKSNLSTQFHLLLGMGFKKYIDTLKISKSIEML 210

Qy        119 ------IGKIHDVLGLG---------------PDVYLGAYTRY--YTGLLDALADDVVA 154
                   | :| : ||                  |: |  |  :|  | | |  |   |||
Db        211 LTTTKTISQISETLGFSNVSTYSRQFKNYLSVTPNAY-RAMKKYDKYNGCSD---DDV-- 264

Qy        155 DRGEEAAAAVDELVARFLPMLKLLTFDQ 182
                |  : |  |:   :|  :|  :|:
Db        265 --SEHLKSCVQSLICSKMPTNELDNYDE 290


RESULT 5
US-11-045-802-29
; Sequence 29, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
```

```
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 655
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-11-045-802-29

  Query Match             8.0%;  Score 75;  DB 7;  Length 655;
  Best Local Similarity   22.4%;  Pred. No. 4.4;
  Matches   35;  Conservative   23;  Mismatches   50;  Indels   48;  Gaps    7;

Qy         41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-TQAEY 99
              | | :  || | :    :       |:|   : :||          | :|::|  |: ||
Db        314 GYDKEDKAARAYDLAALKYWGTTTTTNF--PMSNYE----------KELEEMKHMTRQEY 361

Qy        100 LLGL---------GRGEY-----DTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL 145
              :  |         |  :|       ::   :||||::       |:||| ::
Db        362 IAHLRRNSSGFSRGASKYRGVTRHHQHGRWQARIGRVAG----NKDIYLGTFS------- 410

Qy        146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
                    |||| | |    :|  :  :  ||
Db        411 ----------TEEEAAEAYDIAAIKFRGLNAVTNFD 436


RESULT 6
US-11-045-802-30
; Sequence 30, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 581
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-11-045-802-30

  Query Match             7.9%;  Score 74;  DB 7;  Length 581;
  Best Local Similarity   23.7%;  Pred. No. 4.7;
  Matches   37;  Conservative   18;  Mismatches   53;  Indels   48;  Gaps    7;

Qy         41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-TQAEY 99
              | | :  || | :    :       |:|   |  ||          | ||::|  |: ||
Db        245 GYDKEEKAARAYDLAALKYWGTTTTTNF--PLSEYE----------KEVEEMKHMTRQEY 292

Qy        100 LL-------GLGRG-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL 145
              :        |  ||           ::   :||||::       |:||| :
Db        293 VASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTF-------- 340

Qy        146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
                    |||| | |    :|  :  :  ||
Db        341 ---------GTQEEAAEAYDIAAIKFRGLSAVTNFD 367
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```
RESULT 7
US-11-045-802-31
; Sequence 31, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 584
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-11-045-802-31

  Query Match             7.9%;  Score 74;  DB 7;  Length 584;
  Best Local Similarity   23.7%;  Pred. No. 4.7;
  Matches   37;  Conservative   18;  Mismatches   53;  Indels   48;  Gaps    7;

Qy         41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-TQAEY 99
              | | :  || | :    :       |:|   |  ||          | ||::|  |: ||
Db        248 GYDKEEKAARAYDLAALKYWGPTTTTNF--PLSEYE----------KEVEEMKHMTRQEY 295

Qy        100 LL-------GLGRG-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL 145
              :        |  ||           ::   :||||::       |:||| :
Db        296 VASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTF-------- 343

Qy        146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
                    |||| | |    :|  :  :  ||
Db        344 ---------GTQEEAAEAYDIAAIKFRGLSAVTNFD 370


RESULT 8
US-11-045-802-32
; Sequence 32, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 579
;   TYPE: PRT
;   ORGANISM: Brassica napus
US-11-045-802-32

  Query Match             7.8%;  Score 73;  DB 7;  Length 579;
  Best Local Similarity   23.1%;  Pred. No. 5.8;
  Matches   36;  Conservative   19;  Mismatches   53;  Indels   48;  Gaps    7;
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Qy          41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-TQAEY 99
               | | :  || | :    :       |:|   :  ||          | ||::|  |: ||
Db         248 GYDKEEKAARAYDLAALKYWGTTTTTNF--PMSEYE----------KEVEEMKHMTRQEY 295

Qy         100 LL-------GLGRG-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL 145
               :       |  ||          ::   :||||::        |:||| :
Db         296 VASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTF-------- 343

Qy         146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
                        |||| | |    :|  :  :  ||
Db         344 ---------GTQEEAAEAYDIAAIKFRGLTAVTNFD 370


RESULT 9
US-10-858-730-292
; Sequence 292, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
;  APPLICANT: Bailey, Richard B.
;  APPLICANT:  Blomquist, Paul
;  APPLICANT:  Doten, Reed
;  APPLICANT:  Driggers, Edward M.
;  APPLICANT:  Madden, Kevin T.
;  APPLICANT:  O'Leary, Jessica
;  APPLICANT:  O'Toole, George
;  APPLICANT:  Trueheart, Joshua
;  APPLICANT:  Walbridge, Michael J.
;  APPLICANT:  Yorgey, Peter S.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE: 14184-030001
;  CURRENT APPLICATION NUMBER: US/10/858,730
;  CURRENT FILING DATE:  2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/475,000
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: US 60/551,860
;  PRIOR FILING DATE: 2004-03-10
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
;   LENGTH: 610
;   TYPE: PRT
;   ORGANISM: Corynebacterium  glutamicum
US-10-858-730-292

  Query Match             7.8%;  Score 72.5;  DB 1;  Length 610;
  Best Local Similarity   26.5%;  Pred. No. 6.8;
  Matches   31;  Conservative   13;  Mismatches   56;  Indels   17;  Gaps    4;

Qy          14 RNGIDGHALADRIGLDEAEIAWRL----SFTGIDDDTMAALAAEQPLFEATADALVTDFY 69
               | | ||  |    | :   : | :       | |:  :   |  : |     | | |
Db         503 RRGEDGRFLWPGFGDNSRVLKWVIDRIEGHVGADETVVGHTAKAEDL---DLDGLDTPIE 559

Qy          70 DHLESYERTQDLFANSTKTVEQLKETQAEYLLGLG---RGEYDTEYAAQRARIGKIH 123
               |  |:     : :||         |  ||||  ||     |  ::: | :|||   |
Db         560 DVKEALTAPAEQWANDV-------EDNAEYLTFLGPRVPAEVHSQFDALKARISAAH 609


RESULT 10
US-11-045-802-33
; Sequence 33, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 579
;   TYPE: PRT
;   ORGANISM: Brassica napus
US-11-045-802-33

  Query Match             7.7%;  Score 72;  DB 7;  Length 579;
  Best Local Similarity   22.4%;  Pred. No. 7.1;
  Matches   35;  Conservative   20;  Mismatches   53;  Indels   48;  Gaps    7;

Qy          41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-TQAEY 99
               | | :  || | :    :       |:|   :  ||          | :|::|  |: ||
Db         248 GYDKEEKAARAYDLAALKYWGTTTTTNF--PMSEYE----------KEIEEMKHMTRQEY 295

Qy         100 LL-------GLGRG-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL 145
               :       |  ||          ::   :||||::        |:||| :
Db         296 VASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTF-------- 343

Qy         146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
                        |||| | |    :|  :  :  ||
Db         344 ---------GTQEEAAEAYDIAAIKFRGLTAVTNFD 370


RESULT 11
US-10-858-730-72
; Sequence 72, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
;  APPLICANT: Bailey, Richard B.
;  APPLICANT:  Blomquist, Paul
;  APPLICANT:  Doten, Reed
;  APPLICANT:  Driggers, Edward M.
;  APPLICANT:  Madden, Kevin T.
;  APPLICANT:  O'Leary, Jessica
;  APPLICANT:  O'Toole, George
;  APPLICANT:  Trueheart, Joshua
;  APPLICANT:  Walbridge, Michael J.
;  APPLICANT:  Yorgey, Peter S.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE: 14184-030001
;  CURRENT APPLICATION NUMBER: US/10/858,730
;  CURRENT FILING DATE:  2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/475,000
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: US 60/551,860
;  PRIOR FILING DATE: 2004-03-10
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis
US-10-858-730-72

  Query Match             7.6%;  Score 71;  DB 1;  Length 1192;
  Best Local Similarity   26.5%;  Pred. No. 21;
  Matches   31;  Conservative   16;  Mismatches   34;  Indels   36;  Gaps    6;

Qy          57 FEATADALVTDFY----DHLESY---ERTQDLFANSTKTVEQLKE-----TQAEYLLG-L 103
               ||| |||: |: :     :|  |   :| :||     |    :: :     :  |:|| :
Db          68 FEAGADAVETNTFGCNLSNLGDYDIADRIRDLSQKGTAIARRVADELGSPDRKRYVLGSM 127

Qy         104 GRGEY-----DTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVAD 155
               | |       ||||  |                   |||    |:||  || :: :
Db         128 GPGTKLPTLGHTEYAVIR-----------------DAYTEAALGMLDGGADAILVE 166
```

```
RESULT 12
US-10-858-730-67
; Sequence 67, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
;  APPLICANT: Bailey, Richard B.
;  APPLICANT:  Blomquist, Paul
;  APPLICANT:  Doten, Reed
;  APPLICANT:  Driggers, Edward M.
;  APPLICANT:  Madden, Kevin T.
;  APPLICANT:  O'Leary, Jessica
;  APPLICANT:  O'Toole, George
;  APPLICANT:  Trueheart, Joshua
;  APPLICANT:  Walbridge, Michael J.
;  APPLICANT:  Yorgey, Peter S.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE: 14184-030001
;  CURRENT APPLICATION NUMBER: US/10/858,730
;  CURRENT FILING DATE:  2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/475,000
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: US 60/551,860
;  PRIOR FILING DATE: 2004-03-10
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
;   LENGTH: 530
;   TYPE: PRT
;   ORGANISM: Streptomyces coelicolor
US-10-858-730-67

  Query Match             7.6%;  Score 70.5;  DB 1;  Length 530;
  Best Local Similarity   21.8%;  Pred. No. 8.8;
  Matches   47;  Conservative   24;  Mismatches   72;  Indels   73;  Gaps   10;

Qy          6 DTLVTADVRNGIDGHALADRIGLDEAE------------------IAWR---------LS 38
              ||:|        | |:: : : ||:||                  :  |         :
Db        285 DTIVPDSANQPYDMHSVIEHV-LDDAEFFETQPLFAPNILTGFGRVEGRPVGIVANQPMQ 343

Qy         39 FTGIDDDTMAALAAEQPLFEATADAL---VTDFYD---HLESYERTQD---------LFA 83
              | |  | | :  ||    |  | ||     |  | |     ::  |          :||
Db        344 FAGCLDITASEKAAR---FVRTCDAFNVPVLTFVDVPGFLPGVDQEHDGIIRRGAKLIFA 400

Qy         84 NSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLG---LGPDVYLGAYTRY 140
               :  ||  :                    |   | :||:|   || |: |   |
Db        401 YAEATVPLIT------------------VITRKAFGGAYDVMGSKHLGADLNLAWPTAQ 441

Qy        141 YT-----GLLDALADDVVADRGEEAAAAVDELVARF 171
                  | :: |    :|| |::| |    |:  :
Db        442 IAVMGAQGAVNILHRRTIADAGDDAEATRARLIQEY 477


RESULT 13
US-11-045-802-28
; Sequence 28, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 597
;   TYPE: PRT
;   ORGANISM: oryza sativa
US-11-045-802-28

  Query Match             7.6%;  Score 70.5;  DB 7;  Length 597;
  Best Local Similarity   23.1%;  Pred. No. 10;
  Matches   33;  Conservative   17;  Mismatches   42;  Indels   51;  Gaps    6;

Qy         69 YDHLESYERTQDLFA--------------NSTKTVEQLKE-TQAEYLL-------GLGR 105
              ||  |   |  || |              |  | :|::|  |: |::         |  |
Db        224 YDKEEKAARAYDLAALKYWGPTTTTNFPVNNYEKELEEMKHMTRQEFVASLRRKSSGFSR 283

Qy        106 G-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGE 158
              |            ::   :||||::        |:||| ::                  |
Db        284 GASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTFSTQ----------------E 322

Qy        159 EAAAAVDELVARFLPMLKLLTFD 181
              ||| | |    :|  :  :  ||
Db        323 EAAEAYDIAAIKFRGLNAVTNFD 345


RESULT 14
US-11-045-802-26
; Sequence 26, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
;  APPLICANT: Gordon-Kamm, William
;  APPLICANT:  Helentjaris, Tim
;  APPLICANT:  Lowe, Keith
;  APPLICANT:  Shen, Bo
;  APPLICANT:  Tarczynski, Mitchell
;  APPLICANT:  Zheng, Peizhong
;  TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
;  TITLE OF INVENTION:  and Methods of Use
;  FILE REFERENCE: 035718/286074
;  CURRENT APPLICATION NUMBER: US/11/045,802
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: 60/541,122
;  PRIOR FILING DATE: 2004-02-02
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-11-045-802-26

  Query Match             7.6%;  Score 70.5;  DB 7;  Length 692;
  Best Local Similarity   23.1%;  Pred. No. 12;
  Matches   33;  Conservative   17;  Mismatches   42;  Indels   51;  Gaps    6;

Qy         69 YDHLESYERTQDLFA--------------NSTKTVEQLKE-TQAEYLL-------GLGR 105
              ||  |   |  || |              |  | :|::|  |: |::         |  |
Db        319 YDKEEKAARAYDLAALKYWGPTTTTNFPVNNYEKELEEMKHMTRQEFVASLRRKSSGFSR 378

Qy        106 G-------EYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGE 158
              |            ::   :||||::        |:||| ::                  |
Db        379 GASIYRGVTRHHQHGRWQARIGRVAG----NKDLYLGTFSTQ----------------E 417

Qy        159 EAAAAVDELVARFLPMLKLLTFD 181
              ||| | |    :|  :  :  ||
Db        418 EAAEAYDIAAIKFRGLNAVTNFD 440


RESULT 15
US-11-082-389-90
; Sequence 90, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
```

```
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-131CPCN
;  CURRENT APPLICATION NUMBER: US/11/082,389
;  CURRENT FILING DATE:  2005-03-16
;  PRIOR APPLICATION NUMBER: US 09/603024
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: US 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 60/143262
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: US 60/151281
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19930487.4
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19930489.0
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931549.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931550.7
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932134.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 90
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-082-389-90

  Query Match             7.4%;  Score 69.5;  DB 7;  Length 360;
  Best Local Similarity   23.7%;  Pred. No. 6.8;
  Matches   45;  Conservative   33;  Mismatches   81;  Indels   31;  Gaps   10;

Qy          2 SNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATA 61
              ||:     ||     :|   |     ::  |:   : ::|    |:  |     |   |:
Db         35 SNNKSAKTTA-----LDNVTLT----VEPGEVIGIIGYSGAGKSTLVRLI--NGLDSPTS 83

Qy         62 DALV---TDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEY-----A 113
               :|:   ||     ||  : : | :|     :|    |:       |  ||  |      |
Db         84 GSLLLNGTDIVGMPES--KLRKLRSNIGMIFQQFNLFQSR--TAAGNVEYPLEVAKMDKA 139

Qy        114 AQRARIGKIHDVLGLG------PDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVD-E 166
              |::||: :: : :|||      |:   |   :   |:  ||| :      :|| :|:| |
Db        140 ARKARVQEMLEFVGLGDKGKNYPEQLSGG-QKQRVGIARALATNPTLLLADEATSALDPE 198

Qy        167 LVARFLPMLK 176
                  | :|:
Db        199 TTHEVLELLR 208


Search completed: November 23, 2005, 05:09:26
Job time : 3.23403 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:37:11 ; Search time 18.0446 Seconds
(without alignments)
843.041 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....DELVARFLPMLKLLTFDQQI 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94.5	10.1	396	2	US-09-902-540-10455	Sequence 10455, A
2	91.5	9.8	955	1	US-08-428-414A-3	Sequence 3, Appli
3	89	9.5	955	1	US-08-006-676B-1	Sequence 1, Appli
4	89	9.5	955	1	US-08-282-845-2	Sequence 2, Appli
5	89	9.5	955	4	PCT-US94-00324-1	Sequence 1, Appli
6	86.5	9.3	318	2	US-09-710-262E-14	Sequence 14, Appl
7	85.5	9.2	302	2	US-09-328-352-4846	Sequence 4846, Ap
8	83.5	8.9	319	2	US-09-489-039A-8872	Sequence 8872, Ap
9	83.5	8.9	640	2	US-10-241-602B-31	Sequence 31, Appl
10	82.5	8.8	831	2	US-09-605-703B-1396	Sequence 1396, Ap
11	82	8.8	329	2	US-10-622-064-28	Sequence 28, Appl
12	82	8.8	542	2	US-09-252-991A-21396	Sequence 21396, A
13	81.5	8.7	1253	2	US-09-252-991A-30019	Sequence 30019, A
14	80.5	8.6	700	2	US-09-252-991A-19384	Sequence 19384, A
15	80	8.6	553	2	US-09-252-991A-32970	Sequence 32970, A
16	80	8.6	677	2	US-09-252-991A-18102	Sequence 18102, A
17	79	8.5	438	2	US-09-540-236-2595	Sequence 2595, Ap
18	79	8.5	592	2	US-09-902-540-15457	Sequence 15457, A
19	79	8.5	878	2	US-08-941-936-2	Sequence 2, Appli
20	78.5	8.4	733	2	US-09-328-352-5599	Sequence 5599, Ap
21	78.5	8.4	755	4	PCT-US93-07923-3	Sequence 3, Appli
22	78.5	8.4	759	4	PCT-US93-07923-2	Sequence 2, Appli
23	78.5	8.4	766	1	US-08-230-491A-3	Sequence 3, Appli
24	78.5	8.4	766	1	US-08-619-280A-3	Sequence 3, Appli
25	78.5	8.4	766	1	US-08-940-391-3	Sequence 3, Appli
26	78.5	8.4	766	2	US-09-794-236-1	Sequence 1, Appli
27	78.5	8.4	766	2	US-10-002-593-6	Sequence 6, Appli
28	78.5	8.4	766	2	US-09-949-016-6146	Sequence 6146, Ap
29	78.5	8.4	766	2	US-09-265-606-3	Sequence 3, Appli
30	78.5	8.4	766	2	US-10-423-714-6	Sequence 6, Appli
31	78.5	8.4	775	2	US-09-949-016-10450	Sequence 10450, A
32	78	8.4	267	2	US-09-902-540-14634	Sequence 14634, A
33	78	8.4	443	2	US-09-328-352-6943	Sequence 6943, Ap
34	78	8.4	510	2	US-09-489-039A-11123	Sequence 11123, A
35	78	8.4	595	2	US-09-902-540-16334	Sequence 16334, A
36	77.5	8.3	331	2	US-09-605-703B-1398	Sequence 1398, Ap
37	77.5	8.3	343	2	US-09-902-540-9727	Sequence 9727, Ap
38	77.5	8.3	629	2	US-09-902-540-12912	Sequence 12912, A
39	77	8.3	297	2	US-09-252-991A-17492	Sequence 17492, A
40	77	8.3	320	2	US-09-252-991A-21006	Sequence 21006, A
41	76.5	8.2	579	2	US-09-252-991A-18063	Sequence 18063, A
42	76	8.1	531	2	US-08-976-063E-34	Sequence 34, Appl
43	76	8.1	620	2	US-09-252-991A-19796	Sequence 19796, A
44	76	8.1	638	2	US-09-477-962-105	Sequence 105, App
45	75.5	8.1	522	2	US-09-134-000C-4946	Sequence 4946, Ap

ALIGNMENTS

RESULT 1
US-09-902-540-10455
; Sequence 10455, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10455
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10455

Query Match 10.1%; Score 94.5; DB 2; Length 396;
Best Local Similarity 23.3%; Pred. No. 0.028;
Matches 40; Conservative 28; Mismatches 81; Indels 23; Gaps 5;

```
Qy         32 EIAWRLSFTGIDDDTMAAL-AAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVE 90
              |:   : |:  |:  :  | |  :| |    |       ||| :  :|  :        |
Db          8 ELKRYVGFSSADEQALVTLHATAKPHFARFARV----FYDRILEHEGARQALEGGESQVG 63

Qy         91 QLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT---RYYTGLLDA 147
                |: |   ::  | || :|  | | | |||::|  : |       ||      : :   :||
Db         64 HLRGTLQVWMDQLLRGPWDEVYYALRCRIGRMHVRIALPQHYMFGAMNILRQEFNSHIDA 123

Qy        148 -LADDVVADRGEEAAAAV-------------DELVARFLPMLKLLTFDQQI 184
               ::  | |   :|                 ::|:|:     :| || | :
Db        124 TYLEEPAALRAARSAVGKILDLELAIMLHTYREDLLAQQARSERLSTFGQLV 175
```

RESULT 2
US-08-428-414A-3
; Sequence 3, Application US/08428414A
; Patent No. 5912166
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: LEISHMANIASIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY

```
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/428,414A
;      FILING DATE:  21-APR-1995
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kadlecek, Ann T.
;      REGISTRATION NUMBER:  39,244
;      REFERENCE/DOCKET NUMBER:  210121.407
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANDBERRY
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  955 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-428-414A-3

  Query Match             9.8%;  Score 91.5;  DB 1;  Length 955;
  Best Local Similarity   27.3%;  Pred. No. 0.24;
  Matches   54;  Conservative   22;  Mismatches   77;  Indels   45;  Gaps    8;

Qy         13 VRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVT---DFY 69
              ||  :|    ::|  |                 : |:| |  ||   |   ||| |
Db        530 VRRRLDAEIASEREKL--------------ESTVAQLEREQRERERVALDALQTHQRKLQ 574

Qy         70 DHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTE-YAAQRARIGKIHDVLGL 128
              : ||| |||    |   : ::|| | |:|    | :   | |       ||   :    |
Db        575 EALESSERTA---AERDQLLQQLTELQSE-RTQLSQVVTDRERLTRDLQRIQYEYGETEL 630

Qy        129 GPDVYLGA----YTRYYTGLL------------DALADDVVADRGEEAAAAVDELV--- 168
                || | |      ||:  :               ||| :  :|:| | ||| :|
Db        631 ARDVALCAAQEMEARYHAAVFHLQTLLELATEWEDALRERALAERDEAAAAELDAAASTS 690

Qy        169 --ARFLPMLKLLTFDQQI 184
                ||     :| : :||:
Db        691 QNARESACERLTSLEQQL 708


RESULT 3
US-08-006-676B-1
; Sequence 1, Application US/08006676B
; Patent No. 5411865
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven
;    TITLE OF INVENTION:  Diagnosis of Leishmaniasis
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jeffrey B. Oster
;      STREET:  8339 SE 57th Street
;      CITY:  Mercer Island
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98040-4906
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatable
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,676B
;      FILING DATE:  15-JAN-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oster, Jeffrey B.
;      REGISTRATION NUMBER:  32,585
;      REFERENCE/DOCKET NUMBER:  REED-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 232 7845
;      TELEFAX:  (206) 236 0205
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  955 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-006-676B-1

  Query Match             9.5%;  Score 89;  DB 1;  Length 955;
  Best Local Similarity   29.3%;  Pred. No. 0.46;
  Matches   49;  Conservative   19;  Mismatches   69;  Indels   30;  Gaps    7;

Qy         44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
              : |:| |  ||    |   ||| |      : ||| |||    |   : ::|| | |:|
Db        546 ESTVAQLEREQRERERVALDALQTHQRKLQEALESSERTA---AERDQLLQQLTELQSE-R 601

Qy        101 LGLGRGEYDTE-YAAQRARIGKIHDVLGLGPDVYLGA----YTRYYTGLL---------- 145
                | :   | |       ||   :    |  || | |      ||:  :
Db        602 TQLSQVVTDRERLTRDLQRIQYEYGETELARDVALCAAQEMEARYHAAVFHLQTLLELAT 661

Qy        146 ---DALADDVVADRGEEAAAAVDELV-----ARFLPMLKLLTFDQQI 184
                  ||| :  :|:| | ||| :|       ||     :| : :||:
Db        662 EWEDALRERALAERDEAAAAELDAAASTSQNARESACERLTSLEQQL 708


RESULT 4
US-08-282-845-2
; Sequence 2, Application US/08282845
; Patent No. 5719263
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    TITLE OF INVENTION:  A 230Kd Antigen Present in Leishmania
;    TITLE OF INVENTION:  Species
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Macintosh Operating System 7.1
;      SOFTWARE:  Microsoft Word for Macintosh 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/282,845
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/006,676
;      FILING DATE:  JANUARY 15, 1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  5004-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  955 amino acids
```

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-282-845-2

  Query Match             9.5%;  Score 89;  DB 1;  Length 955;
  Best Local Similarity   29.3%;  Pred. No. 0.46;
  Matches   49;  Conservative   19;  Mismatches   69;  Indels   30;  Gaps    7;

Qy         44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
              : |:| |  ||   |   ||| |      : ||| |||    |   : ::|| | |:|
Db        546 ESTVAQLEREQRREREVALDALQTHQRKLQEALESSERTA---AERDQLLQQLTELQSE-R 601

Qy        101 LGLGRGEYDTE-YAAQRARIGKIHDVLGLGPDVYLGA----YTRYYTGLL---------- 145
                | :   | |       ||   :    |  || | |      ||:  :
Db        602 TQLSQVVTDRERLTRDLQRIQYEYGETELARDVALCAAQEMEARYHAAVFHLQTLLELAT 661

Qy        146 ---DALADDVVADRGEEAAAAVDELV-----ARFLPMLKLLTFDQQI 184
                 ||| :  :|:| | ||| :|        ||     :| : :||:
Db        662 EWEDALRERALAERDEAAAAELDAAASTSQNARESACERLTSLEQQL 708


RESULT 5
PCT-US94-00324-1
; Sequence 1, Application PC/TUS9400324
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven
;    TITLE OF INVENTION:  Diagnosis of Leishmaniasis
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word, version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/00324
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,676
;      FILING DATE:  15-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  5004-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  955 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-00324-1

  Query Match             9.5%;  Score 89;  DB 4;  Length 955;
  Best Local Similarity   29.3%;  Pred. No. 0.46;
  Matches   49;  Conservative   19;  Mismatches   69;  Indels   30;  Gaps    7;

Qy         44 DDTMAALAAEQPLFEATADALVT---DFYDHLESYERTQDLFANSTKTVEQLKETQAEYL 100
              : |:| |  ||   |   ||| |      : ||| |||    |   : ::|| | |:|
Db        546 ESTVAQLEREQRREREVALDALQTHQRKLQEALESSERTA---AERDQLLQQLTELQSE-R 601

Qy        101 LGLGRGEYDTE-YAAQRARIGKIHDVLGLGPDVYLGA----YTRYYTGLL---------- 145
                | :   | |       ||   :    |  || | |      ||:  :

Db        602 TQLSQVVTDRERLTRDLQRIQYEYGETELARDVALCAAQEMEARYHAAVFHLQTLLELAT 661

Qy        146 ---DALADDVVADRGEEAAAAVDELV-----ARFLPMLKLLTFDQQI 184
                 ||| :  :|:| | ||| :|        ||     :| : :||:
Db        662 EWEDALRERALAERDEAAAAELDAAASTSQNARESACERLTSLEQQL 708


RESULT 6
US-09-710-262E-14
; Sequence 14, Application US/09710262E
; Patent No. 6887694
; GENERAL INFORMATION:
;  APPLICANT: Rosenberg, Eugene
;  APPLICANT:  Ron, Eliora
;  APPLICANT:  Orr, Elisha
;  APPLICANT:  Paitan, Yossi
;  TITLE OF INVENTION: GENE CLUSTER
;  FILE REFERENCE: 2290.00076
;  CURRENT APPLICATION NUMBER: US/09/710,262E
;  CURRENT FILING DATE:  2000-11-10
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 318
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-710-262E-14

  Query Match             9.3%;  Score 86.5;  DB 2;  Length 318;
  Best Local Similarity   26.4%;  Pred. No. 0.17;
  Matches   34;  Conservative   15;  Mismatches   55;  Indels   25;  Gaps    3;

Qy         73 ESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVL------ 126
              :||   ::||   |    || |   ::   ||    :  | |: ||:  : |||
Db         22 QSYFMAKELFDTQTGFKRQLLELDEQFKQRLGHSILERIYDARAARLDPLDDVLVSFPAI 81

Qy        127 -------------GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
                          |: ||  :||       |:|  :  |       ||  :| ||
Db         82 FMIEHALARLLIDRGIQPDAVVGASMGEVAAA--AIAGAISVDAAVALVAAQAQLFARTA 139

Qy        173 P---MLKLL 178
                |   || :|
Db        140 PRGGMLAVL 148


RESULT 7
US-09-328-352-4846
; Sequence 4846, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4846
;   LENGTH: 302
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-4846

  Query Match             9.2%;  Score 85.5;  DB 2;  Length 302;
  Best Local Similarity   29.4%;  Pred. No. 0.21;
  Matches   37;  Conservative   23;  Mismatches   41;  Indels   25;  Gaps    7;

Qy         25 RIGL---DEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDL 81
              ||||   | ||:   |   |  ::|:  |    | : |    | :||:| :  |  : |
Db        179 RIGLSNVDSAELIKSLP-QGPHNNTLVYL---DPPYYAKGQDLYRNFYNHQDHVEIMRAL 234

Qy         82 FANSTK-------TVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGK-----IHDVLGLG 129
                ::| |        |: ::|   :: :     ||  :| ||: :||:      :||  |
```

```
Db        235 KSSSIKNWIVSYDNVDAIREIYKDFRV----LEYSLQYTAQQKKIGEEVMIFSNDV--LI 288

Qy        130 PDVYLG 135
              |:| ||
Db        289 PNVRLG 294


RESULT 8
US-09-489-039A-8872
; Sequence 8872, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 8872
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8872

  Query Match             8.9%;  Score 83.5;  DB 2;  Length 319;
  Best Local Similarity   25.4%;  Pred. No. 0.39;
  Matches   51;  Conservative   17;  Mismatches   72;  Indels   61;  Gaps    9;

Qy         14 RNGIDGHALADRIGLDEAEIA-WRLSFTGIDDDTMAALAAEQPLF-------EATADALV 65
              |  |||  |    |:||| :| ||        ||:  :| : | |       |     |:
Db        120 RRNIDGVVLFGFTGIDEAMLAPWR--------DTLVLMARDAPGFASVCYDDEGAITLLM 171

Qy         66 TDFYDH--------------LESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTE 111
                ||                : : ||    :    |   :|  | |   ||: :| |||
Db        172 QRLYDRGHRHISFLGVPHSDVTTGERRHLAYLAFCKK-HRLTPTAALPGLGMKQG-YDTV 229

Qy        112 YAAQRARIGKI---HDVLGLGPDVYLGAYTRYYTGLLDAL-------------------- 148
               :   |    :    | | ||   ||     |       |||
Db        230 ASVLTAETSALVCATDTLALGASKYLQQQGR------DALQLASVGSTPLMKFLHPEILT 283

Qy        149 ADDVVADRGEEAAAAVDELVA 169
               |   |: |  ||  : | :|
Db        284 VDPGYAESGRRAARQLIEQIA 304


RESULT 9
US-10-241-602B-31
; Sequence 31, Application US/10241602B
; Patent No. 6887989
; GENERAL INFORMATION:
;  APPLICANT: Simard, Nathalie
;  APPLICANT:  Brouwers, Huub
;  APPLICANT:  Jones, Simon
;  APPLICANT:  Griffiths, Steve
;  APPLICANT:  Valenzuela, Pablo
;  APPLICANT:  Burzio, Luis
;  TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
;  FILE REFERENCE: H-32319A
;  CURRENT APPLICATION NUMBER: US/10/241,602B
;  CURRENT FILING DATE:  2002-09-11
;  PRIOR APPLICATION NUMBER: PCT/GB01/01055
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: GB0005838.8
;  PRIOR FILING DATE: 2000-03-11
;  PRIOR APPLICATION NUMBER: GB0016080.4
;  PRIOR FILING DATE: 2000-07-01
;  PRIOR APPLICATION NUMBER: GB0016082.0
;  PRIOR FILING DATE: 2000-07-01
;  PRIOR APPLICATION NUMBER: GB0018599.1
;  PRIOR FILING DATE: 2000-07-29
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 640
;   TYPE: PRT
;   ORGANISM: Piscirickettsia salmonis
US-10-241-602B-31

  Query Match             8.9%;  Score 83.5;  DB 2;  Length 640;
  Best Local Similarity   20.4%;  Pred. No. 1.1;
  Matches   38;  Conservative   31;  Mismatches   92;  Indels   25;  Gaps    4;

Qy          2 SNDNDTLVTADVRNG----------IDGHALAD----RIGLDEAEIAWRLSFTGI----- 42
              : || | ||  |  |          :    |||      |: : |: : :   ||
Db        428 AQDNQTAVTVHVLQGEREVATGNKSLGRFDLADIPPAPRGMPQVEVTFDIDANGILNVSA 487

Qy         43 -----DDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQA 97
                  :    : |   | :   ||:: |  || :  :: |:|          :  |:
Db        488 KDKGTGKEQSIVIRASSGLSDDEVDAMIKDAEDHADDDKKFQELVGARNNAEAMIHATEK 547

Qy         98 EYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRG 157
                    :   | : | ::| | :: ||:       :       |     :|: : |::|
Db        548 GLKEAGDKVAADDKTAIEKA-ISELKDVVSGNDKAVIDEKVEALTQASAKMAEVLYANQG 606

Qy        158 EEAAAA 163
                 || ||
Db        607 AEAEAA 612


RESULT 10
US-09-605-703B-1396
; Sequence 1396, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: BGI-129CP
;  CURRENT APPLICATION NUMBER: US/09/605,703B
;  CURRENT FILING DATE:  2000-06-27
;  PRIOR APPLICATION NUMBER: 60/142,764
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 60/152,318
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1396
;   LENGTH: 831
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1396

  Query Match             8.8%;  Score 82.5;  DB 2;  Length 831;
  Best Local Similarity   25.4%;  Pred. No. 2.1;
  Matches   46;  Conservative   25;  Mismatches   81;  Indels   29;  Gaps    8;

Qy          7 TLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVT 66
              |||   | ||     | |:   |  |:  |  :  ::| :   :| :  |     |   :
Db        486 TLVA--VFNG----QLLDQHQRDYEEV--RAMYIALNDRSNLEIARDLGL-----DNKDS 532

Qy         67 DFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEY-DTEYAAQRARIGKIHDV 125
              :||:   : || :|: |   : ||  :  | :       | ||   : | ||    : |
Db        533 EFYEVYRAIERDRDVMAGDQQRVESERRQQLQQEYEANREEYVMAKIAEQRVEYDRRH-- 590

Qy        126 LGLGP--DVYLGAYTRYYTGLLDALADDVV--------ADRGEEAAAAVDELVARFLPML 175
                  |    | |  |  | | |   :|          |  || | ||   ::    |::
Db        591 ---MPRHTASLEAVGRELTSLRDRTIEDYTARMNTLRRARAGERANAAESRIIDELRPIV 647

Qy        176 K 176
               :
```

```
Db        648 E 648


RESULT 11
US-10-622-064-28
; Sequence 28, Application US/10622064
; Patent No. 6932971
; GENERAL INFORMATION:
;  APPLICANT: Bachmann, Martin F
;  APPLICANT:  Maurer, Patrik F
;  TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
;  FILE REFERENCE: 1700.0300001
;  CURRENT APPLICATION NUMBER: US/10/622,064
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 60/396,575
;  PRIOR FILING DATE: 2002-07-18
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Bacteriophage SP
US-10-622-064-28

  Query Match             8.8%;  Score 82;  DB 2;  Length 329;
  Best Local Similarity   24.5%;  Pred. No. 0.61;
  Matches   39;  Conservative   17;  Mismatches   61;  Indels   42;  Gaps    6;

Qy         37 LSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANS----------T 86
              ||||     |    ||   : |     || |: |  |:|         | |:|
Db         93 LSFTSYSTDEERALIRTE-LAALLADPLIVDAIDNLNPAYWAALLVASSGGGDNPSDPDV 151

Qy         87 KTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLG-PDVYLGAYTRYYTGLL 145
                | :|          | | |   :|     |:| |::|    | ||:|
Db        152 PVVPDVKPPD-------GTGRYKCPFACY--RLGSIYEVGKEGSPDIY------------ 190

Qy        146 DALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQI 184
                      :||:| :   |  :  ||       :||::
Db        191 ---------ERGDEVSVTFDYALEDFLGNTNWRNWDQRL 220


RESULT 12
US-09-252-991A-21396
; Sequence 21396, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 21396
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21396

  Query Match             8.8%;  Score 82;  DB 2;  Length 542;
  Best Local Similarity   25.3%;  Pred. No. 1.3;
  Matches   49;  Conservative   19;  Mismatches   66;  Indels   60;  Gaps    8;

Qy          3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD 62
              |:|||:|| ::| |                          |:||:||| |   | ||
Db        149 NENDTVVTDEIRFG-------------------------DNDTLAALVAN--LVEADLL 180

Qy         63 ALVTD---FYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQR--A 117
                ::||    :|          |   :     ||          ||||   |:  | |  |

Db        181 VILTDRDGMFDADPRNNPDAQLIYEARADDPQLDAVAGGSAGALGRGGMQTKLRAARLAA 240

Qy        118 RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVA----------DRGEEAAAAVDEL 167
              | |         |  | :|       | :: : | : |          ||  :||    :
Db        241 RSG--------GHTVIVG-------GRIERVLDRLRAGERLGTLLTPDRSRKAAR--KQW 283

Qy        168 VARFLPMLKLLTFD 181
              :|  | |   |  |
Db        284 LAGHLQMRGTLVLD 297


RESULT 13
US-09-252-991A-30019
; Sequence 30019, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 30019
;   LENGTH: 1253
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30019

  Query Match             8.7%;  Score 81.5;  DB 2;  Length 1253;
  Best Local Similarity   22.5%;  Pred. No. 5.1;
  Matches   48;  Conservative   31;  Mismatches   75;  Indels   59;  Gaps   11;

Qy          2 SNDNDTLVTAD-VRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEAT 60
              | |:|  : |: : : :||     |:|:: |        |:| | : |       |:
Db       1024 SGDHDRQLHAEFLEHALDGE--DRRLGVEGVE-------DGLDQDQVGA------AFDQA 1068

Qy         61 ADALVTDFYDHLESYERTQDLF---------------ANSTKTVEQLKETQAEYLLGLG 104
              | |     :  :|       :                    :  : | |   :  :| | |
Db       1069 AGRLDVVLHQFVEGDVAVAGVVHVRGNRAGAAGRAEHAGDEARLVRGLGGLRVRHLAGQA 1128

Qy        105 RGEYDTEYAAQRARIGKIHDVLGLG----------PDVYLGAYTRYYTGLLDALADDVVA 154
              |  :: |:  ||      :| |:|||          ||  |       |||| | | | |
Db       1129 R-PFEVEFVGQR-----LHAVVGLGHLGGVEGVGLEDVGAGV----EVGLLDGL-DHVRA 1177

Qy        155 DRGEEAAAA------VDELVARFLPMLKLLTFD 181
              : :|   |       | | :|  : : :|:  |
Db       1178 AQQQEVVVAFHVARPVGEALAAVVGLFQLVALD 1210


RESULT 14
US-09-252-991A-19384
; Sequence 19384, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 19384
;   LENGTH: 700
;   TYPE: PRT
```

```
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19384

  Query Match             8.6%;  Score 80.5;  DB 2;  Length 700;
  Best Local Similarity   24.6%;  Pred. No. 2.8;
  Matches   49;  Conservative   21;  Mismatches   82;  Indels   47;  Gaps    8;

Qy          12 DVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALV---TDF 68
               | |    | | :  :    :| :| |          |:|  || | |  | |  :    | :
Db         129 DARRPADAHPVVGQRAF-QATLAQR-------QVTVATAAAGQRLALAAAGDVAQHRTQY 180

Qy          69 YDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKI-HDVLG 127
                :| :  |:  :   :          |  |  | ||||||   ::|   |  | : | ||
Db         181 AEHQDQDEQHAEHLLDDVPEPRLRVERNAVDLFGLGRGERRVDHADAVAAAGVVAHRVL- 239

Qy         128 LGPDVYLGAYTRYYTGLLDALAD------DV--------------------VADRGEE- 159
                     |      | : |    :||      |:                   ||||  :
Db         240 -----YQAGEARQFVGAPGLVADLAGLRVDLHLVVQHHRHRQSAQASLLLLGVADRAVQF 294

Qy         160 -AAAAVDELVARFLPMLKL 177
                 |  :  || |    |:|
Db         295 VVAGGLVALVGRVRRQLRL 313


RESULT 15
US-09-252-991A-32970
; Sequence 32970, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 32970
;   LENGTH: 553
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32970

  Query Match             8.6%;  Score 80;  DB 2;  Length 553;
  Best Local Similarity   21.1%;  Pred. No. 2.2;
  Matches   41;  Conservative   28;  Mismatches   79;  Indels   46;  Gaps    5;

Qy          20 HALADRI-----GLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLES 74
               || | |:      ||   :    :  |:  | : | | ::||    |::       |  :
Db         137 HAPAPRLLVSAFFLDAPAVGLGPAVEGLAVDEVVAQAGQRPLRSFFAESAEEQRVIHRAA 196

Qy          75 YERTQDLFANSTKTVEQLKETQAE----YLLGLGRGEYDTEYAAQ-------RARIGK-- 121
                    |         :    : ||      ::||  |:   |  ||       | |:|:
Db         197 LHALQQFLDQGLVVLRGDAQAQAPAHQVEVVGLVEGQEQVEAGAQFVHFHQWRQRLGQGG 256

Qy         122 ---------------------IHDVL-------GLGPDVYLGAYTRYYTGLLDALADDVV 153
                                   : ||:       |:|| |   |  |:  |:   :|: :
Db         257 QVPMGDRYLVAEGVAAGVVGVVADVIGVEIVEEGVGPVVEGNAEDRHVVGVHHPVAEAIG 316

Qy         154 ADRGEEAAAAVDEL 167
                  |:|   |:|:|
Db         317 LPAGDEFGVALDDL 330


Search completed: November 23, 2005, 04:51:24
Job time : 23.0446 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:50:03 ; Search time 60.1486 Seconds
(without alignments)
1278.178 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....DELVARFLPMLKLLTFDQQI 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	10.6	448	4	US-10-460-524-5	Sequence 5, Appli
2	97.5	10.5	138	4	US-10-767-701-34787	Sequence 34787, A
3	94.5	10.1	883	4	US-10-369-493-18563	Sequence 18563, A
4	94	10.1	218	4	US-10-156-761-9281	Sequence 9281, Ap
5	89.5	9.6	400	4	US-10-156-761-13480	Sequence 13480, A
6	89.5	9.6	400	5	US-10-732-923-10618	Sequence 10618, A
7	88	9.4	505	4	US-10-282-122A-66025	Sequence 66025, A
8	87	9.3	496	4	US-10-282-122A-65364	Sequence 65364, A
9	86.5	9.3	318	5	US-10-848-111-14	Sequence 14, Appl
10	86	9.2	362	4	US-10-437-963-137315	Sequence 137315,
11	85	9.1	2703	4	US-10-282-122A-66108	Sequence 66108, A
12	84	9.0	163	4	US-10-425-115-287808	Sequence 287808,
13	84	9.0	258	4	US-10-425-115-287807	Sequence 287807,
14	83.5	8.9	258	4	US-10-156-761-11335	Sequence 11335, A
15	83.5	8.9	315	4	US-10-282-122A-59961	Sequence 59961, A
16	83.5	8.9	367	4	US-10-425-114-72593	Sequence 72593, A
17	83.5	8.9	368	4	US-10-425-114-48921	Sequence 48921, A
18	83.5	8.9	640	5	US-10-913-883-31	Sequence 31, Appl
19	83.5	8.9	1254	4	US-10-282-122A-53778	Sequence 53778, A
20	83.5	8.9	4384	5	US-10-472-928-3658	Sequence 3658, Ap
21	83	8.9	319	6	US-11-097-143-13032	Sequence 13032, A
22	83	8.9	384	4	US-10-425-114-48636	Sequence 48636, A
23	82.5	8.8	403	4	US-10-282-122A-61978	Sequence 61978, A
24	82.5	8.8	695	4	US-10-282-122A-69832	Sequence 69832, A
25	82.5	8.8	765	4	US-10-369-493-13529	Sequence 13529, A
26	82.5	8.8	831	3	US-09-738-626-5468	Sequence 5468, Ap
27	82.5	8.8	928	4	US-10-282-122A-61748	Sequence 61748, A
28	82.5	8.8	939	4	US-10-156-761-12605	Sequence 12605, A
29	82	8.8	318	4	US-10-425-114-63899	Sequence 63899, A
30	82	8.8	329	4	US-10-243-739-16	Sequence 16, Appl
31	82	8.8	329	4	US-10-244-065-16	Sequence 16, Appl
32	82	8.8	329	4	US-10-289-454-16	Sequence 16, Appl
33	82	8.8	329	4	US-10-346-190-16	Sequence 16, Appl
34	82	8.8	329	4	US-10-465-811-7	Sequence 7, Appli
35	82	8.8	329	4	US-10-289-456-16	Sequence 16, Appl
36	82	8.8	329	4	US-10-622-064-28	Sequence 28, Appl
37	82	8.8	329	4	US-10-622-124-10	Sequence 10, Appl
38	82	8.8	329	4	US-10-622-087-10	Sequence 10, Appl
39	82	8.8	329	6	US-11-037-396-10	Sequence 10, Appl
40	82	8.8	330	4	US-10-050-902-254	Sequence 254, App
41	82	8.8	330	4	US-10-050-898-254	Sequence 254, App
42	82	8.8	901	4	US-10-369-493-18812	Sequence 18812, A
43	82	8.8	1333	4	US-10-282-122A-55546	Sequence 55546, A
44	82	8.8	2799	4	US-10-282-122A-65564	Sequence 65564, A
45	81	8.7	1178	4	US-10-128-714-8240	Sequence 8240, Ap

ALIGNMENTS

RESULT 1
US-10-460-524-5
; Sequence 5, Application US/10460524
; Publication No. US20040029781A1
; GENERAL INFORMATION:
; APPLICANT: Hernan, Ronald A
; APPLICANT: Mehigh, Richard J
; APPLICANT: Brockie, Ian
; APPLICANT: Jenkins, Elizabeth
; TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant Prot
; FILE REFERENCE: SGM 7047.1
; CURRENT APPLICATION NUMBER: US/10/460,524
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/388,059
; PRIOR FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Streptococcus
US-10-460-524-5

Query Match 10.6%; Score 99; DB 4; Length 448;
Best Local Similarity 25.3%; Pred. No. 0.31;
Matches 48; Conservative 25; Mismatches 45; Indels 72; Gaps 8;

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Qy          10 TADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDD-------DTMAALAAE--------- 53
               |  :||| :   | : :|  |  :| |   :   |        ||:|| |||
Db          41 TPIIRNGGE---LTNLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGAAAWEA 97

Qy          54 ----QPLFEATADAL-------VTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
                    | :| ||||       |:|:| :|          |: |||| :|: ||: :
Db          98 AAAADALAKAKADALKEFNKYGVSDYYKNL----------INNAKTVEGIKDLQAQVV-- 145

Qy         103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
                       :|::||| :  |                   || | |     |   |:
Db         146 ---------ESAKKARISEATD-----------------GLSDFLKSQTPA---EDTVK 175

Qy         163 AVDELVARFL 172
               :::   |: |
Db         176 SIELAEAKVL 185
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RESULT 2
US-10-767-701-34787
; Sequence 34787, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

```
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 34787
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-C54418_1.pep
US-10-767-701-34787

  Query Match             10.5%;  Score 97.5;  DB 4;  Length 138;
  Best Local Similarity   24.1%;  Pred. No. 0.095;
  Matches   28;  Conservative   26;  Mismatches   57;  Indels    5;  Gaps    2;

Qy         27 GLDEAEIAWRLSFTGIDDDT----MAALAAEQPLFEATADALVTDFYDHLESYERTQDLF 82
              |:|:|| |     : :  :|    | ||  :  | : |   ||    :| :       | :
Db          3 GMDKAEDAEPTCISSVQKETGHKVMDALEQQDALLKKTKSLLVPSVLNHHDDIPGEADNY 62

Qy         83 ANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYT 138
                ::  |:|    ||::|:     :|     : |:  ::| | :::   || |:  :|
Db         63 MDALNTLESETETESEFQT-KNQGVPAPSFNAEAPQVGAIDNIVPQCPDSYVADFT 117


RESULT 3
US-10-369-493-18563
; Sequence 18563, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18563
;   LENGTH: 883
;   TYPE: PRT
;   ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-18563

  Query Match             10.1%;  Score 94.5;  DB 4;  Length 883;
  Best Local Similarity   28.3%;  Pred. No. 2.2;
  Matches   51;  Conservative   23;  Mismatches   63;  Indels   43;  Gaps   10;

Qy         12 DVRNGIDGH--ALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEA-------TAD 62
              ||:: ::|    |||:|   : | |          :  :| : |:   |||       | |
Db        180 DVKSNVEGQLDRLADQIA--DKEAADPHDRLASHNTALAEVTADIEHFEAEREQARQTRD 237

Qy         63 ALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRA----- 117
                | | || || ::   |:  :|:  ::|  ||        | : |  | |
Db        238 ----DAADVLERYEESRTALADVEETIADVREAVAE-------AERERETLADRVSDHRE 286

Qy        118 RIGKIHDV-------LGL-GPDVYLGAYTRYYTGLLDALAD--DVVADRGEEAAAAVDEL 167
              |   : |        |||  ||    :  |      ||:||  : ||:|  | | ||  |
Db        287 RASDLDDEAAALAADLGLDDPDAEDASAER------DAVADQREAVAERVREVAPAVSRL 340


RESULT 4
US-10-156-761-9281
; ; Sequence 9281, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9281
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-9281

  Query Match             10.1%;  Score 94;  DB 4;  Length 218;
  Best Local Similarity   28.7%;  Pred. No. 0.39;
  Matches   47;  Conservative   22;  Mismatches   73;  Indels   22;  Gaps    8;

Qy         21 ALADRIGLDEAEI--AWRLSF-TGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYER 77
              |||||:|:  ||:    |||  :|: :  : || : :|  |    |    |   |:   |
Db         25 ALADRLGVAHAEVFDVGRLSVASGVPEPVVKALLSGRPAGEPDLQA---RFLQRLDLLRR 81

Qy         78 TQDLFANSTKTVEQ-------LKETQAEYLLGLGRGEYDTEYAAQRARIGKIHD--VLGL 128
              |: |  |  :  :|       :   ||  |:  |       |:    |  ::|   :
Db         82 TR-LKPNRRRYTQQEIADGAGMSRQQAGALIN-GDRRPTMEHCDAIQRFFRVHAGFLTAE 139

Qy        129 GPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
              |:  |   |    ||  |     |||   || |||: : | |
Db        140 DPEALAGTLQRSEQELLQQL-----ADRERAAAMAVDDPLERLL 178


RESULT 5
US-10-156-761-13480
; Sequence 13480, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13480
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-13480

  Query Match              9.6%;  Score 89.5;  DB 4;  Length 400;
  Best Local Similarity   26.7%;  Pred. No. 2.5;
  Matches   36;  Conservative   16;  Mismatches   66;  Indels   17;  Gaps    5;

Qy         42 IDDDTMAALAAEQPLFEATADALVTDFYDHLESY--ERTQDLFANSTKTVEQLKETQAEY 99
```

```
                : : : | : |  |   |    :   ||| | :   |  :|||        |   || :
Db          2 LSEQSAATVRATLPAVGAAVGEITARFYDRLFAARPELLRDLFNRG----NQAAGTQRQA 57

Qy        100 LLG--LGRGEYDTEYAAQRA-----RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152
              | |       |  |: :|      ||   |  ||: | |   :   : : : | | |
Db         58 LAGSIAAFATYLVEHPDERPDAMLDRIAHKHASLGIAPGQYAVVHEHLFAAIAEVLGDAV 117

Qy        153 VADRGEEAAAAVDEL 167
                 | ||| ||:
Db        118 T----PEVAAAWDEV 128


RESULT 6
US-10-732-923-10618
; Sequence 10618, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
;  APPLICANT: Edgerton, Michael D
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
;  FILE REFERENCE: 38-15(52796)C
;  CURRENT APPLICATION NUMBER: US/10/732,923
;  CURRENT FILING DATE:  2003-12-10
;  PRIOR APPLICATION NUMBER: 10/310,154
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 10618
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis MA-4680
US-10-732-923-10618

  Query Match             9.6%;  Score 89.5;  DB 5;  Length 400;
  Best Local Similarity   26.7%;  Pred. No. 2.5;
  Matches   36;  Conservative   16;  Mismatches   66;  Indels   17;  Gaps    5;

Qy         42 IDDDTMAALAAEQPLFEATADALVTDFYDHLESY--ERTQDLFANSTKTVEQLKETQAEY 99
                : : : | : |  |   |    :   ||| | :   |  :|||        |   || :
Db          2 LSEQSAATVRATLPAVGAAVGEITARFYDRLFAARPELLRDLFNRG----NQAAGTQRQA 57

Qy        100 LLG--LGRGEYDTEYAAQRA-----RIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152
              | |       |  |: :|      ||   |  ||: | |   :   : : : | | |
Db         58 LAGSIAAFATYLVEHPDERPDAMLDRIAHKHASLGIAPGQYAVVHEHLFAAIAEVLGDAV 117

Qy        153 VADRGEEAAAAVDEL 167
                 | ||| ||:
Db        118 T----PEVAAAWDEV 128


RESULT 7
US-10-282-122A-66025
; Sequence 66025, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66025
;   LENGTH: 505
;   TYPE: PRT
;   ORGANISM: Neisseria meningitidis
US-10-282-122A-66025

  Query Match             9.4%;  Score 88;  DB 4;  Length 505;
  Best Local Similarity   25.7%;  Pred. No. 4.8;
  Matches   46;  Conservative   24;  Mismatches   69;  Indels   40;  Gaps    7;

Qy          6 DTLVTADVRNGIDGHALADRIGLDEAEIAWRLSF---TGIDDDTMAALAAEQPLF----- 57
              | |  |  | | :    :|  |       |:|:       |:   |  || : ||
Db        325 DQLALAIGRGGQNVRLASDLTG-------WQLNIMTSAEADERNAAEDAAIRRLFMDHLN 377

Qy         58 --EATADALVTDFYDHLE--SYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYA 113
                | ||| || : :  ||  :|    :| |      :|   |   : |    |    |
Db        378 VDEETADVLVQEGFATLEEVAYVPAAELLA-----IEGFDEEIVDMLRNRARDAILTMAI 432

Qy        114 AQRARIGKIHDVL----GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELV 168
              |   ::|:: | :    |:  |              :| :||:  :  | : |  |||||:
Db        433 AAEEKLGEVSDDMRNLEGIDAD-----------MLRSLAEAGITTRDDLAELAVDELI 479


RESULT 8
US-10-282-122A-65364
; Sequence 65364, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
```

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;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65364
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65364

  Query Match             9.3%;  Score 87;  DB 4;  Length 496;
  Best Local Similarity   25.7%;  Pred. No. 5.9;
  Matches   46;  Conservative   24;  Mismatches   69;  Indels   40;  Gaps    7;

Qy          6 DTLVTADVRNGIDGHALADRIGLDEAEIAWRLSF---TGIDDDTMAALAAEQPLF----- 57
              | |  |  | | :    :|  |       |:|:       |:   |  || : ||
Db        316 DRLALAIGRGGQNVRLASDLTG-------WQLNIMTSAEADERNAAEDAAIRRLFMNHLN 368

Qy         58 --EATADALVTDFYDHLE--SYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYA 113
                | ||| || : :  ||  :|    :| |     :|   |   : |     |     |
Db        369 VDEETADVLVQEGFATLEEVAYVPAAELLA-----IEGFDEEIVDMLRNRARDAILTMAI 423

Qy        114 AQRARIGKIHDVL----GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELV 168
              |   ::|:: | :    |:  |: |           :||:  :  | : |  |||||:
Db        424 AAEEKLGEVSDDMRNLEGVDADMLL-----------SLAEAGITTRDDLAELAVDELI 470


RESULT 9
US-10-848-111-14
; Sequence 14, Application US/10848111
; Publication No. US20040235107A1
; GENERAL INFORMATION:
;  APPLICANT: Rosenberg, Eugene
;  APPLICANT:  Ron, Eliora
;  APPLICANT:  Orr, Elisha
;  APPLICANT:  Paitan, Yossi
;  TITLE OF INVENTION: GENE CLUSTER
;  FILE REFERENCE: 27757
;  CURRENT APPLICATION NUMBER: US/10/848,111
;  CURRENT FILING DATE:  2004-05-19
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 318
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-10-848-111-14

  Query Match             9.3%;  Score 86.5;  DB 5;  Length 318;
  Best Local Similarity   26.4%;  Pred. No. 3.7;
  Matches   34;  Conservative   15;  Mismatches   55;  Indels   25;  Gaps    3;

Qy         73 ESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVL------ 126
              :||   ::||   |   || |   ::   ||    :  | |: ||:  : |||
Db         22 QSYFMAKELFDTQTGFKRQLLELDEQFKQRLGHSILERIYDARAARLDPLDDVLVSFPAI 81

Qy        127 --------------GLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL 172
                           |: ||  :||          |:|  :  |       ||  :| ||
Db         82 FMIEHALARLLIDRGIQPDAVVGASMGEVAAA--AIAGAISVDAAVALVAAQAQLFARTA 139

Qy        173 P---MLKLL 178
              |   || :|
Db        140 PRGGMLAVL 148


RESULT 10
US-10-437-963-137315
; Sequence 137315, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 137315
;   LENGTH: 362
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_3880C.1.pep
US-10-437-963-137315

  Query Match             9.2%;  Score 86;  DB 4;  Length 362;
  Best Local Similarity   26.4%;  Pred. No. 5;
  Matches   51;  Conservative   20;  Mismatches   78;  Indels   44;  Gaps    9;

Qy          8 LVTADVRNGIDGHALADRIGLDEAEIAWR----LSFT--GIDDDTMAALAAEQPLFEATA 61
              :: ||   |  |  ||  ||::  |   |    | ||  |  |     :  |: |:::|
Db         26 ILAADESTGTIGKRLAS-IGVENVEENRRALRELLFTAPGALDCLSGVILFEETLYQSTR 84

Qy         62 DALVTDFYDHLESY---------ERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEY 112
              |   | | | | :         : | :|     :|  |  :         | ||    |
Db         85 DG--TPFVDVLAAAGVLAGIKVDKGTVELAGTDRETTTQGHD---------GLGERCRRY 133

Qy        113 AAQRARIGKIHDVLGLG----------PDVYLGAYTRY-----YTGLLDALADDVVAD-- 155
              |  ||  |   || :|           |        ||        ||:  :  ::: |
Db        134 YAAGARFAKWRAVLSIGRASSRPSQLAVDANAQGLARYAIICQENGLVPIVEPEILVDGE 193

Qy        156 RGEEAAAAVDELV 168
              | || | | | |
Db        194 HGIEACAEVTERV 206


RESULT 11
US-10-282-122A-66108
; Sequence 66108, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
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;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66108
;   LENGTH: 2703
;   TYPE: PRT
;   ORGANISM: Neisseria meningitidis
US-10-282-122A-66108

  Query Match             9.1%;  Score 85;  DB 4;  Length 2703;
  Best Local Similarity   23.5%;  Pred. No. 88;
  Matches   52;  Conservative   26;  Mismatches   71;  Indels   72;  Gaps    9;

Qy          3 NDNDTLVTADVRNGIDGHAL--------ADRIGLDEAEIAWRLSFTGIDDDT-------- 46
              :| |:   :  |:|:: | :          | |    |   |: :|||| :|
Db       2153 SDGDS-KNSTTRSGVNTHNIHITDEAGQLARTGRTAKETEARI-YTGIDTETADQHSGHL 2210

Qy         47 -----MAALAAEQPLFE----------ATADALVTDFYDHLESYERTQDLFANSTKTVEQ 91
                  |:| |  |             | | | | |   : :|||| |:     |    :
Db       2211 KNSFDKDAVAKEINLQREVTKEFGRNAAQAVAAVADKLGNTQSYERYQEA---RTLLEAE 2267

Qy         92 LKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVL------------GLGPDVYLGAYT 138
              |: | :|           | || || :|:::  |            |:|  :  ||
Db       2268 LQNTDSE----------AEKAAFRASLGQVNAYLAENQSRYDTWKEGGIGRSILHGAAG 2316

Qy        139 RYYTGLLDAL------------ADDVVADRGEEAAAAVDEL 167
                || |  :             |    : |    |||: |
Db       2317 GLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGKAAVNAL 2357


RESULT 12
US-10-425-115-287808
; Sequence 287808, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 287808
;   LENGTH: 163
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_25575C.1.pep
US-10-425-115-287808

  Query Match             9.0%;  Score 84;  DB 4;  Length 163;
  Best Local Similarity   25.6%;  Pred. No. 2.8;
  Matches   31;  Conservative   25;  Mismatches   43;  Indels   22;  Gaps    5;

Qy         58 EATADALVTDF-YDHLESYERTQDLFANSTKTVEQLKE-------TQAEYLLGLGRGEYD 109
              :| :|| :| : |  | ||    |:| :|  : :||::       || : :  :|  ||
Db         46 KANSDAPITAYRYHSLCSYMGDDDMF-SSDLSEDQLRQRLGHMSTTQCQVIFSMG-DEYV 103

Qy        110 TEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVA 169
               ||  :|| : ::   ||    | :              :  :::| :||  |: : |
Db        104 PEYVDKRALVDRLCRALGGAEKVEI-----------EWGNHALSNRVQEAVVAIVDFVK 151

Qy        170 R 170
               |
Db        152 R 152


RESULT 13
US-10-425-115-287807
; Sequence 287807, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 287807
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_25574C.1.pep
US-10-425-115-287807

  Query Match             9.0%;  Score 84;  DB 4;  Length 258;
  Best Local Similarity   25.6%;  Pred. No. 5.1;
  Matches   31;  Conservative   25;  Mismatches   43;  Indels   22;  Gaps    5;

Qy         58 EATADALVTDF-YDHLESYERTQDLFANSTKTVEQLKE-------TQAEYLLGLGRGEYD 109
              :| :|| :| : |  | ||    |:| :|  : :||::       || : :  :|  ||
Db        141 KANSDAPITAYRYHSLCSYMGDDDMF-SSDLSEDQLRQRLGHMSTTQCQVIFSMG-DEYV 198

Qy        110 TEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVA 169
               ||  :|| : ::   ||    | :              :  :::| :||  |: : |
Db        199 PEYVDKRALVDRLCRALGGAEKVEI-----------EWGNHALSNRVQEAVVAIVDFVK 246

Qy        170 R 170
               |
Db        247 R 247


RESULT 14
US-10-156-761-11335
; Sequence 11335, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
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;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11335
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Streptomyces avermitilis
US-10-156-761-11335

  Query Match             8.9%;  Score 83.5;  DB 4;  Length 258;
  Best Local Similarity   24.1%;  Pred. No. 5.7;
  Matches   49;  Conservative   21;  Mismatches   78;  Indels   55;  Gaps    9;

Qy          8 LVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTD 67
              :| ||| :   | |||  ||     :       | :||  ||:            :  |
Db         33 VVVADVLDD-QGEALAKEIGARYVHLD-----VGREDDWQAAV-----------TVAKD 74

Qy         68 FYDHLESYE------RTQDLFANSTKTVEQLKE-TQAEYLLGLGRGEYDTEYAAQRARIG 120
               | |::         | ||        :|: :  |    ||:     : | ||    |
Db         75 AYGHIDGLVNNAGILRFNDLVGTPLAEFQQIVQVNQVGVFLGIKTVAPEIE-AAGGGTIV 133

Qy        121 KIHDVLGLGPDVYLGAYT-----------------------RYYTGLLD-ALADDVVA 154
                 ||    |:||||                         | :| |:::
Db        134 NTASYAGLTGMAYVGAYTATKHAIVGLTRVAALELAAKKIRVNAVCPGAIDTAMSNPSQL 193

Qy        155 DRG---EEAAAAVDELVARFLPM 174
              | |   || | |: ||  | :|:
Db        194 DPGADPEETARALSELYGRLVPL 216


RESULT 15
US-10-282-122A-59961
; Sequence 59961, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1

; SEQ ID NO 59961
;   LENGTH: 315
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59961

  Query Match             8.9%;  Score 83.5;  DB 4;  Length 315;
  Best Local Similarity   25.4%;  Pred. No. 7.4;
  Matches   51;  Conservative   17;  Mismatches   72;  Indels   61;  Gaps    9;

Qy         14 RNGIDGHALADRIGLDEAEIA-WRLSFTGIDDDTMAALAAEQPLF-------EATADALV 65
              |  |||  |    |:||| :| ||         ||:  :| : | |        |     |:
Db        116 RRNIDGVVLFGFTGIDEAMLAPWR--------DTLVLMARDAPGFASVCYDDEGAITLLM 167

Qy         66 TDFYDH--------------LESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTE 111
                ||                : : ||    :    |   :|  | |   ||: :| |||
Db        168 QRLYDRGHRHISFLGVPHSDVTTGERRHLAYLAFCKK-HRLTPTAALPGLGMKQG-YDTV 225

Qy        112 YAAQRARIGKI---HDVLGLGPDVYLGAYTRYYTGLLDAL-------------------- 148
               :   |    :    | | ||   ||    |      |||
Db        226 ASVLTAETSALVCATDTLALGASKYLQQQGR------DALQLASVGSTPLMKFLHPEILT 279

Qy        149 ADDVVADRGEEAAAAVDELVA 169
               |   |: |  ||  : | :|
Db        280 VDPGYAESGRRAARQLIEQIA 300


Search completed: November 23, 2005, 05:09:02
Job time : 61.1486 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:50:08 ; Search time 7.26597 Seconds
(without alignments)
203.984 Million cell updates/sec

Title: US-09-455-978B-2
Perfect score: 2394
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....ATDQQVRTVEEVRETVGKLS 489

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169.5	7.1	1448	1	US-10-485-517-212	Sequence 212, App
2	160	6.7	364	1	US-10-984-376-5	Sequence 5, Appli
3	160	6.7	364	1	US-10-984-376-6	Sequence 6, Appli
4	160	6.7	1279	1	US-10-793-626-3188	Sequence 3188, Ap
5	150.5	6.3	3717	1	US-10-821-234-1076	Sequence 1076, Ap
6	147.5	6.2	691	1	US-10-131-826A-16	Sequence 16, Appl
7	147.5	6.2	703	1	US-10-821-234-963	Sequence 963, App
8	142.5	6.0	667	1	US-10-821-234-1477	Sequence 1477, Ap
9	141	5.9	614	7	US-11-074-176-80	Sequence 80, Appl
10	141	5.9	706	1	US-10-485-517-146	Sequence 146, App
11	140.5	5.9	989	1	US-10-821-234-975	Sequence 975, App
12	139.5	5.8	1586	1	US-10-821-234-901	Sequence 901, App
13	137.5	5.7	1095	1	US-10-793-626-3154	Sequence 3154, Ap
14	134.5	5.6	5024	1	US-10-793-626-2964	Sequence 2964, Ap
15	134	5.6	284	1	US-10-821-234-1632	Sequence 1632, Ap
16	133.5	5.6	1290	1	US-10-485-517-141	Sequence 141, App
17	132.5	5.5	877	7	US-11-074-176-322	Sequence 322, App
18	132.5	5.5	883	7	US-11-074-176-88	Sequence 88, Appl
19	132.5	5.5	1126	1	US-10-485-517-248	Sequence 248, App
20	131.5	5.5	416	1	US-10-793-626-2	Sequence 2, Appli
21	127	5.3	1107	1	US-10-485-517-145	Sequence 145, App
22	126.5	5.3	585	1	US-10-793-626-2124	Sequence 2124, Ap
23	125	5.2	794	1	US-10-793-626-1050	Sequence 1050, Ap
24	124	5.2	875	1	US-10-858-730-7	Sequence 7, Appli
25	123.5	5.2	539	1	US-10-793-626-888	Sequence 888, App
26	120.5	5.0	1189	7	US-11-074-176-134	Sequence 134, App
27	120	5.0	772	1	US-10-858-730-77	Sequence 77, Appl
28	119.5	5.0	1192	1	US-10-858-730-72	Sequence 72, Appl
29	119	5.0	544	1	US-10-821-234-889	Sequence 889, App
30	118.5	4.9	761	1	US-10-485-517-252	Sequence 252, App
31	118.5	4.9	1140	1	US-10-858-730-208	Sequence 208, App
32	118	4.9	718	7	US-11-074-176-306	Sequence 306, App
33	118	4.9	723	7	US-11-074-176-18	Sequence 18, Appl
34	117	4.9	581	1	US-10-793-626-28	Sequence 28, Appl
35	117	4.9	598	7	US-11-082-389-398	Sequence 398, App
36	117	4.9	752	1	US-10-793-626-1036	Sequence 1036, Ap
37	117	4.9	1299	1	US-10-821-234-1145	Sequence 1145, Ap
38	117	4.9	1572	1	US-10-793-626-2906	Sequence 2906, Ap
39	116	4.8	1992	7	US-11-013-759-3	Sequence 3, Appli
40	116	4.8	1992	7	US-11-013-759-13	Sequence 13, Appl
41	116	4.8	2047	7	US-11-013-759-4	Sequence 4, Appli
42	116	4.8	2047	7	US-11-013-759-7	Sequence 7, Appli
43	115.5	4.8	495	1	US-10-821-234-1154	Sequence 1154, Ap
44	115.5	4.8	776	1	US-10-821-234-1171	Sequence 1171, Ap
45	115	4.8	615	1	US-10-982-545-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-485-517-212
; Sequence 212, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 212
; LENGTH: 1448
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-212

Query Match 7.1%; Score 169.5; DB 1; Length 1448;
Best Local Similarity 20.8%; Pred. No. 0.0083;
Matches 115; Conservative 95; Mismatches 197; Indels 147; Gaps 26;

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Qy          11 ADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYD 70
               ||: |    : : :    :|| ||       |  |    ||:| :             |
Db           7 ADIDNAAANNDVDNAKTTNEATIA------AITPDANVKPAAKQAI------------AD 48

Qy          71 HLESYERTQDLFANSTKTVE---------QLKETQAEYLLGLGRGEYDTEYAAQRARIGK 121
                ::: |   |   |:  | |          | ::| |:  :       : | ||::| | |
Db          49 KVQAQETAID--GNNGSTTEEKAAAKQQVQTEKTTADAAIDAAHTNAEVE-AAKKAAIAK 105

Qy         122 IHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFD 181
               |  :          :  |   |  | : :| :  |   |: :                 T 137
Db         106 IEAI------------QPATTTKDN-AKEAIATKANERKTAIAQ--------------

Qy         182 QQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTD 241
               | |  :    : |     ::|:    ||   :::||       | ||:  ::  |    :
Db         138 QDITAEEIAAANA-----DVDNAVTQAN---SNIEA------ANSQNDVDQAKTTGENSI 183

Qy         242 DQ----VDRMADVSREISSV-SASVEEVASTAD--DVRRTSEDAEALAQQGEA-AADDAL 293
               ||    |:: |    ||::: :  ::|: :| |  |  : : ||||  : |:|  |  |
Db         184 DQVTPTVNKKATARNEITAILNNKLQEIQATPDATDEEKQAADAEANTENGKANQAISAA 243
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Qy        294 ATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDI-AEQTNML--ALNASIEAARAG- 349
Db        244 TTNAQVDEAKANAEAAINAVTPKVVKKQAAKDEIDQLQATQTNVINNDQNATTEEKEAAI 303

Qy        350 --------EAGEGFAVVADE----------------------VKALAEESREQ--STRVE 377
Db        304 QQLATAVTDAKNNITAATDDNGVDQAKDAGKNSIQSTQPATAVKSNAKNDVDQAVTTQNQ 363

Qy        378 ELVEQMQAETEETVDQLDEV------------NQRIGEGVERV-EEAMETLQEIT--DAV 422
Db        364 AIDNTTGATTEEKNAAKDLVLKAKEKAYQDILNAQTTNDVTQIKDQAVADIQGITADTTI 423

Qy        423 EDAASGMQEVSTATDEQA--------VSTEEVAEMVDGVD------DRAGEIAAALDDIA 468
Db        424 KDVAK--DELATKANEQKALIAQTADATTEEKEQANQQVDAQLTQGNQNIENAQSIDDVN 481

Qy        469 DATDQQVRTVEEVR 482
Db        482 TAKDNAIQAIDPIQ 495


RESULT 2
US-10-984-376-5
; Sequence 5, Application US/10984376
; Publication No. US20050244436A1
; GENERAL INFORMATION:
;  APPLICANT: GIULIANI, Marzia Monica
;  APPLICANT:  PIZZA, Mariagrazia
;  APPLICANT:  RAPPUOLI, Rino
;  TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
;  FILE REFERENCE: 2300-1609.20
;  CURRENT APPLICATION NUMBER: US/10/984,376
;  CURRENT FILING DATE:  2004-11-09
;  PRIOR APPLICATION NUMBER: 09/979,263
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: PCT/IB00/00828
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: GB 9911692.3
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: GB 9919705.5
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: GB 0005730.7
;  PRIOR FILING DATE: 2000-03-09
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: representative ORF 961 protein
US-10-984-376-5

  Query Match             6.7%;  Score 160;  DB 1;  Length 364;
  Best Local Similarity   23.5%;  Pred. No. 0.0058;
  Matches   67;  Conservative   45;  Mismatches  119;  Indels   54;  Gaps   11;

Qy        236 MRARTDDQVDRMADVS--------REISSVSASVEEVASTADDVRRTSEDAEALAQQGEA 287
Db         24 LAATSDDDVKKAATVAIVAAYNNGQEINGFKAG-ETIYDIGEDGTITQKDATA----ADV 78

Qy        288 AADD--------ALATMT--------DIDEATDGVTAGVEQLGERAADVESVTGVIDDIA 331
Db         79 EADDFKGLGLKKVVTNLTKTVNENKQNVDAKVKAAESEIEKLTTKLADTDAALADTDAAL 138

Qy        332 EQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETV 391
Db        139 DETTN-ALN---------KLGENITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDIA 188

Qy        392 DQLDEVNQRIGEGVERVEEAMETLQEITDAVE------DAASGMQEVSTATDEQAVSTEE 445
Db        189 DSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAAETAAGKAEAAAGTANTAADKAE 248

Qy        446 VAEMVDGVDDRAGEIAAALDDIA------DATDQQVRTV-EEVRE 483
Db        249 A--VAAKVTDIKADIATNKADIAKNSARIDSLDKNVANLRKETRQ 291


RESULT 3
US-10-984-376-6
; Sequence 6, Application US/10984376
; Publication No. US20050244436A1
; GENERAL INFORMATION:
;  APPLICANT: GIULIANI, Marzia Monica
;  APPLICANT:  PIZZA, Mariagrazia
;  APPLICANT:  RAPPUOLI, Rino
;  TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
;  FILE REFERENCE: 2300-1609.20
;  CURRENT APPLICATION NUMBER: US/10/984,376
;  CURRENT FILING DATE:  2004-11-09
;  PRIOR APPLICATION NUMBER: 09/979,263
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: PCT/IB00/00828
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: GB 9911692.3
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: GB 9919705.5
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: GB 0005730.7
;  PRIOR FILING DATE: 2000-03-09
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: representative ORF 961 protein
US-10-984-376-6

  Query Match             6.7%;  Score 160;  DB 1;  Length 364;
  Best Local Similarity   23.5%;  Pred. No. 0.0058;
  Matches   67;  Conservative   45;  Mismatches  119;  Indels   54;  Gaps   11;

Qy        236 MRARTDDQVDRMADVS--------REISSVSASVEEVASTADDVRRTSEDAEALAQQGEA 287
Db         24 LAATSDDDVKKAATVAIVAAYNNGQEINGFKAG-ETIYDIGEDGTITQKDATA----ADV 78

Qy        288 AADD--------ALATMT--------DIDEATDGVTAGVEQLGERAADVESVTGVIDDIA 331
Db         79 EADDFKGLGLKKVVTNLTKTVNENKQNVDAKVKAAESEIEKLTTKLADTDAALADTDAAL 138

Qy        332 EQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETV 391
Db        139 DETTN-ALN---------KLGENITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDIA 188

Qy        392 DQLDEVNQRIGEGVERVEEAMETLQEITDAVE------DAASGMQEVSTATDEQAVSTEE 445
Db        189 DSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAAETAAGKAEAAAGTANTAADKAE 248

Qy        446 VAEMVDGVDDRAGEIAAALDDIA------DATDQQVRTV-EEVRE 483
Db        249 A--VAAKVTDIKADIATNKADIAKNSARIDSLDKNVANLRKETRQ 291


RESULT 4
US-10-793-626-3188
; Sequence 3188, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
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; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3188

Query Match 6.7%; Score 160; DB 1; Length 1279;
Best Local Similarity 18.1%; Pred. No. 0.023;
Matches 110; Conservative 105; Mismatches 219; Indels 174; Gaps 22;

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Qy          2 SNDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATA 61
              :|:  ||:       | ||:|       || | | :|    :::          | : |:|
Db        629 ANNQKTLI------GNDGNATD-----DEKEAAKQLVTQKLNEQI-------QKIHESTQ 670

Qy         62 DALVTDFYDHLESYERTQDLFANSTKTVEQ--------LKETQAEYLLGLGRGEYDTEYA 113
              |  |    |::::   |     |:     |         | |::   :    |  |
Db        671 DNQV----DNVKAQAITAIKLINANAHKRQDAINILTNLAESKKSDI----RANQDATTE 722

Qy        114 AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGE------------EA 160
               :   |  | | |    :   || |       :|| |: : |  :             :|
Db        723 EKNTAIQSIDDTLAQARNNINGANT-------NALVDENLEDGKQKLQRIVLSTQTKTQA 775

Qy        161 AAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLS 220
              | : : : :          |:  :|   ::  :   : ::   :  | |   ::| |:
Db        776 KADIAQAIGQ----------QRSTIDQNQNATTEEKQEALERLNQETNGVNDRIQAALA 824

Qy        221 SLEATSQ--------------------------DVAERTDTMRARTDDQVD-------R 246
              :   | :                         ||:|  :    |  ::        :
Db        825 NQNVTDEKNNILETIRNVEPIVIVKPKANEIIRKKAAEQTTLINQNQDATLEEKQIALGK 884

Qy        247 MADVSRE-ISSVS----------------ASVEEVASTADDVRRTSEDAEALAQ------ 283
              : :|  | :: ||                | : ||       |   :: |  ||
Db        885 LEEVKNEALNQVSQAHSNNDVKIVENNGIAKISEVHPETIIKRNAKQEIEQDAQSQIDTI 944

Qy        284 --------QGEAAADDA--LATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQ 333
                     : ::|| |   :| :  |:  |:  |  :    : : :  |:: ::   | :
Db        945 NANNKSTNEEKSAAIDRVNVAKIDAINNITNATTTQLVNDAKNSGNT-SISQILPSTAVK 1003

Qy        334 TNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAE--TEETV 391
              || |       || | ||    |::     | |||  | : :|: | |:  |      |
Db       1004 TNAL-------AALASEAKNKNAIIDQTPNATAEEKEEANNKVDRLQEEADANILKAHTT 1056

Qy        392 DQLDEVNQRIGEGVERV-------EEAMETLQEITD------------AVEDAASG---M 429
              |::: :  :  :  |       : |   | :  |             :|: |     :
Db       1057 DEVNNIKNQAVQNINAVQVEVIKKQNAKNQLNQFIDNQKKIIENTPDATLEEKAEANRLL 1116

Qy        430 QEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAA----------ALDDIADATDQQVRTVE 479
              | | |:| ::  : :   |:  :|    :| | |          ||: | :| : | : ::
Db       1117 QNVLTSTSDEIANVDHNNEVDQALDKARPKIEAIVPQVSKKRDALNAIQEAFNSQTQEIQ 1176

Qy        480 EVRETVGK 487
              | :|   :
Db       1177 EKQEATNE 1184
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RESULT 5
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

Query Match 6.3%; Score 150.5; DB 1; Length 3717;
Best Local Similarity 20.7%; Pred. No. 0.24;
Matches 114; Conservative 87; Mismatches 220; Indels 129; Gaps 22;

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Qy         13 VRNGIDGHALADRIG-------LDEAEIAWRL------SFTGIDDDTMAALAAEQPLFEA 59
              |  |  ||::   :        ||: | |  |          ||:  :||     :
Db       2175 VPGGPVGHSIHCEVCDHCVVLLLDDLERAGALLPAIHEQLRGINASSMAWARLHR----- 2229

Qy         60 TADALVTDFYDHLES-----YERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAA 114
                :| : |    | |     :|  | |     : :||   :  :    ||     |  |
Db       2230 -LNASIADLQSQLRSPLGPRHETAQQL-----EVLEQQSTSLGQDARRLGGQAVGTRDQA 2283

Qy        115 QRARIGKIHDVLGLGPDVYLGAYTRYYTGL--LDALADDVVADRGE----EAAAAVDELV 168
                :          | | :  ||        :  :|    :::  |       |:|   | :
Db       2284 SQ---------LLAGTEATLGHAKTLLAAIRAVDRTLSELMSQTGHLGLANASAPSGEQL 2334

Qy        169 ARFLPMLKLLTFDQ--------QIAMDTYIDSYAQRL----HDEIDSRQELANAVATHVE 216
              | |  :: | ::          | | :  : : ||||      ::: |   |   |:||
Db       2335 LRTLAEVERLLWEMRARDLGAPQAAAEAEL-AAAQRLLARVQEQLSSLWEENQALATQTR 2393

Qy        217 APLSSLEATSQDVAE----RTDTMR----------ARTDDQVDRMADVSREISSVSASVE 262
              |:  ||   |: |       | |            | :: : |  ::||: ::: |::
Db       2394 DRLAQHEAGLMDLREALNRAVDATREAQELNSRNQERLEEALQRKQELSRDNATLQATLH 2453

Qy        263 EVASTADDVRR-------TSEDAEALAQQGEAAADDALATMTDIDEA------TDGVTAG 309
                |  | |         |: | ||  : |     |  |       :   |
Db       2454 AARDTLASVFRLLHSLDQAKEELERLAASLDGARTPLLQRMQTFSPAGSKLRLVEAAEAH 2513

Qy        310 VEQLGERAADVESVTGVIDDIAEQTNMLALNAS------IEAARAGEAGEGFA------- 356
              :|||: | :: |:  ::|   ::    |: ||      ::| :| |   | |
Db       2514 AQQLGQLALNLSSI--ILDVNQDRLTQRAIEASNAYSRILQAVQAAEDAAGQALQQADHT 2571

Qy        357 ---VVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAME 413
                 ||   :   |::    || :|| : | |                ||:|     :: |
Db       2572 WATVVRQGLVDRAQQLLANSTALEEAMLQEQ-------------QRLGLVWAALQGART 2617

Qy        414 TLQEI---TDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADA 470
              |:::   | :|       :  |    |: |:| :: :       |  :||   | |
Db       2618 QLRDVRAKKDQLE------AHIQAAQAMLAMDTDETSKKI----AHAKAVAAEAQDTATR 2667

Qy        471 TDQQVRTVEE 480
                |:: ::|
Db       2668 VQSQLQAMQE 2677
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RESULT 6
US-10-131-826A-16
; Sequence 16, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven

```
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 16
;    LENGTH: 691
;    TYPE: PRT
;    ORGANISM: Homo Sapien
US-10-131-826A-16

  Query Match             6.2%;  Score 147.5;  DB 1;  Length 691;
  Best Local Similarity   21.3%;  Pred. No. 0.055;
  Matches  100;  Conservative   74;  Mismatches  171;  Indels  125;  Gaps   21;

Qy          56 LFEATADALVTDFYDHLESY--ERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYA 113
               :|:  | | | |::  : |   | | |       :    : || ||   |   |   |
Db          50 IFKVEA-ACVRDYHTFVWSSVPESTTD-----GSPIHTSVQFQASYLPKPGAQLYQFRYV 103

Qy         114 AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLP 173
                :: :      | |  |      :       :| |     || | :
Db         104 NRQGQ------VCGQSP-----PFQFREPRPMDELVTLEEADGGSDI------------ 139

Qy         174 MLKLLTFDQQIAMDTYIDSYAQRLHD------------EIDSR-QELANAVAT----HV 215
                  ||   :   :  :|   |  :|             |: || |||  |:||    |
Db         140 ---LLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELERALATARQEHT 196

Qy         216 E--APLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRR 273
               |       :  :  :: |  | :  :  | | |: ::  :| ::|   |:| :   :: |
Db         197 ELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTIS---EKVLTKEVELDR 253

Qy         274 TSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQ 333
                 :  :|| :: |                        : || |  || |     :  :|:|
Db         254 LRDTVKALTREQEKL--------------------LGQLKEVQADKEQSEAEL-QVAQQ 291

Qy         334 TNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQ 393
                |   ||  ::                  | |:  ||   |: |::: | ||:       |
Db         292 ENH-HLNLDLK---------------EAKSWQEEQSAQAQRLKDKVAQMK-------DT 327

Qy         394 LDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDE----QAVSTEEVAEM 449
               | :  ||: | :| ::|  :   ||:      |||  |: :   :|     |     :||:
Db         328 LGQAQQRVAE-LEPLKEQLRGAQEL------AASSQQKATLLGEELASAAAARDRTIAEL 380

Qy         450 ------VDGVDDRAGEIAAALDDIADATDQQ----VRTVEEVRETVGKLS 489
                     |  |: |  |:   | :      ::    :::||  :: : |||
Db         381 HRSRLEVAEVNGRLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILKLS 430


RESULT 7
US-10-821-234-963
; Sequence 963, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 963
;    LENGTH: 703
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-821-234-963

  Query Match             6.2%;  Score 147.5;  DB 1;  Length 703;
  Best Local Similarity   21.3%;  Pred. No. 0.056;
  Matches  100;  Conservative   74;  Mismatches  171;  Indels  125;  Gaps   21;

Qy          56 LFEATADALVTDFYDHLESY--ERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYA 113
               :|:  | | | |::  : |   | | |       :    : || ||   |   |   |
Db          62 IFKVEA-ACVRDYHTFVWSSVPESTTD-----GSPIHTSVQFQASYLPKPGAQLYQFRYV 115

Qy         114 AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLP 173
                :: :      | |  |      :       :| |     || | :
Db         116 NRQGQ------VCGQSP-----PFQFREPRPMDELVTLEEADGGSDI------------ 151

Qy         174 MLKLLTFDQQIAMDTYIDSYAQRLHD------------EIDSR-QELANAVAT----HV 215
                  ||   :   :  :|   |  :|             |: || |||  |:||    |
Db         152 ---LLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELERALATARQEHT 208

Qy         216 E--APLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRR 273
               |       :  :  :: |  | :  :  | | |: ::  :| ::|   |:| :   :: |
Db         209 ELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTIS---EKVLTKEVELDR 265

Qy         274 TSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQ 333
                 :  :|| :: |                        : || |  || |     :  :|:|
Db         266 LRDTVKALTREQEKL--------------------LGQLKEVQADKEQSEAEL-QVAQQ 303

Qy         334 TNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQ 393
                |   ||  ::                  | |:  ||   |: |::: | ||:       |
Db         304 ENH-HLNLDLK---------------EAKSWQEEQSAQAQRLKDKVAQMK-------DT 339

Qy         394 LDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDE----QAVSTEEVAEM 449
               | :  ||: | :| ::|  :   ||:      |||  |: :   :|     |     :||:
Db         340 LGQAQQRVAE-LEPLKEQLRGAQEL------AASSQQKATLLGEELASAAAARDRTIAEL 392

Qy         450 ------VDGVDDRAGEIAAALDDIADATDQQ----VRTVEEVRETVGKLS 489
                     |  |: |  |:   | :      ::    :::||  :: : |||
Db         393 HRSRLEVAEVNGRLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILKLS 442


RESULT 8
US-10-821-234-1477
; Sequence 1477, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
```

```
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1477
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1477

  Query Match             6.0%;  Score 142.5;  DB 1;  Length 667;
  Best Local Similarity   19.4%;  Pred. No. 0.098;
  Matches   97;  Conservative   75;  Mismatches  186;  Indels  143;  Gaps   19;

Qy          53 EQPLPEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAE-YLLGLGRGEYDTE 111
               ::|  ::  || : |  | |   | |::  |:| |  :: :  :  |:  ||: |  |
Db         104 DKPSGKSGMDAALDDLIDTLGGPEETEE--ENTTYTGPEVSDPMSSTYIEELGKREV-TI 160

Qy         112 YAAQRARIGKIHDVLG--------LGPDVYLGAYTRYYTGLLDALADD------VVADRG 157
                   |  : |   : |        :|||             :|||: |        | :
Db         161 PPKYRELLAKKEGITGPPADSSKPIGPD-----------DAIDALSSDFTCGSPTAAGKK 209

Qy         158 EEAAAAVDELVARFLPMLKLLTFDQQ----IAMDTYIDSYAQRLHDEIDSRQELANAVAT 213
                 |   : | |:    ::      |:    : || |   : |   : :||
Db         210 TEKEESTEVLKAQSAGTVRSAAPPQEKKRKVEKDTMSDQALEALSASLGTRQ-------A 262

Qy         214 HVEAPLSSLEATSQDVAERTDTMRARTDDQ-----------VDR----MADVSREISSVS 258
                 | | |::   :  |:    :   ||:           |:   :     |
Db         263 EPELDLRSIKEVDEAKAKEEKLEKCGEDDETIPSEYRLKPATDKDGKPLLPEPEEKPKPR 322

Qy         259 ASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEAT-------------- 303
               :  | :   ::|  | ||  |  ::  |   :   |    : ||
Db         323 SESELIDELSEDFDR-SECKEKPSKPTEKTEESKAAAPAPVSEAVCRTSMCSIQSAPPEP 381

Qy         304 ---------DGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEG 354
                        | | |  : ||:: || |    |:| : |:
Db         382 ATLKGTVPDDAVEALADSLGKKEADPEDGKPVMDKVKEKAK------------------ 422

Qy         355 FAVVADEVKALAEESREQSTRVEELVEQMQAETEETVD---QLDEVNQRIGEGV--ERVE 409
                   || ||:                | |||:    :|:|| : |: :  :  :
Db         423 ------------EEDREK-----------LGEKEETIPPDYRLEEVKDKDGKPLLPKESK 459

Qy         410 EAMETLQE--ITDAVEDAASGMQEVSTATDEQ---AVSTEEVAEMVDGVDDRAG------ 458
               | :  : |  : ||: :  || |  |:   |    | :  ||         :||
Db         460 EQLPPMSEDFLLDALSEDFSGPQNASSLKFEDAKLAAAISEVVSQTPASTTQAGAPPRDT 519

Qy         459 -----EIAAALDDIADATDQQ 474
                    ::  ||| ::|:  |:
Db         520 SQSDKDLDDALDKLSDSLGQR 540


RESULT 9
US-11-074-176-80
; Sequence 80, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
;  APPLICANT: Klaenhammer, Todd R.
;  APPLICANT:  Russell, William M.
;  APPLICANT:  Altermann, Eric
;  APPLICANT:  McAuliffe, Olivia
;  APPLICANT:  Peril, Andrea Azcarate
;  TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;  TITLE OF INVENTION:  Stress-Related Proteins and Uses Therefore
;  FILE REFERENCE: 5051-694
;  CURRENT APPLICATION NUMBER: US/11/074,176
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: 60/551,161
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Lactobacillus acidophilus
US-11-074-176-80

  Query Match             5.9%;  Score 141;  DB 7;  Length 614;
  Best Local Similarity   19.8%;  Pred. No. 0.11;
  Matches   98;  Conservative   81;  Mismatches  173;  Indels  142;  Gaps   23;

Qy          43 DDDTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG 102
               |   :| |  :: : | || ||        :|   :|          : :   :
Db         131 DAGKIAGLNVQRIINEPTASAL---------AYGLDKD-----------DDDEKVLVYD 169

Qy         103 LGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAA 162
               || | :|                || ||  |:                  |::  |:
Db         170 LGGGTFDV-------------SVLQLGDGVF-----------------QVLSTNGDTHLG 199

Qy         163 AVDELVARFLPMLKLLTFDQQIAMDTYIDSYA-QRLHDEID-SRQELANAVATHVEAPLS 220
                 |:   | :  | :  |  :  :|    |  | ||| |  : ::::|:   :||:  |
Db         200 G-DDFDNRIMDWL-IKNFKDENGVDLSKDKMAMQRLKDASEKAKKDLSGVSSTHISLPFI 257

Qy         221 S--------LEA---------TSQDVAERTDTM-------RARTDDQVDR--MADVSREI 254
               |        |||           : |: |:|              | : :|:  :    |  |
Db         258 SAGESGPLHLEADLTRAKFDELTNDLVEKTKIPFDNALKDAGLTVNDIDKVILNGGSTRI 317

Qy         255 SSVSASVEEVASTADDVRRTSEDAEALA---QQGEAAADDALATMTDIDEATDGVTAGVE 311
                 :|  :|:|  |      |     ::| ||    | |  : |      : |:      :: |:|
Db         318 PAVQKAVKEWAGKEPDHSINPDEAVALGAAIQGGVISGDVKDIVLLDVTP----LSLGIE 373

Qy         312 QLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESRE 371
                 :|              ||       | ::  | :|  :::    : |:  ||   |:
Db         374 TMG----------GVF------TKLIDRNTTIPTSKS----QIFSTAADNQPAVD----- 408

Qy         372 QSTRVEELVEQMQAETEETVDQLDEVNQRIG----------EGVERVEEAMETLQE--I 418
                     |  :| |      |     :: :|           || :::   :  :  :
Db         409 --------VHVLQGERPMAAD-----DKTLGRFELTDIPPAPRGVPQIQVTFDIDKNGIV 455

Qy         419 TDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALD--DIADATDQQVR 476
                 : :|  :| ::  |       :| ||:  |    :: | |      |  |: :  || :
Db         456 NVSAKDMGTGKEQKITIKSSSGLSDEEIKRMQKDAEEHAEEDKKRKDEADLRNEVDQLIF 515

Qy         477 TVEE-VRETVGKLS 489
               | |: ::|| ||:|
Db         516 TTEKTLKETKGKVS 529


RESULT 10
US-10-485-517-146
; Sequence 146, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
;  APPLICANT: University of Sheffield
;  APPLICANT:  Biosynexus Incorporated
;  APPLICANT:  Foster, Simon
;  APPLICANT:  Mond, James
;  TITLE OF INVENTION: Antigenic Polypeptides
;  FILE REFERENCE: P100629WO
;  CURRENT APPLICATION NUMBER: US/10/485,517
;  CURRENT FILING DATE:  2004-02-02
;  PRIOR APPLICATION NUMBER: GB 0118825.9
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: GB 0200349.9
;  PRIOR FILING DATE: 2002-01-09
;  NUMBER OF SEQ ID NOS: 424
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
;   LENGTH: 706
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-10-485-517-146

  Query Match             5.9%;  Score 141;  DB 1;  Length 706;
```

```
  Best Local Similarity   19.4%;  Pred. No. 0.13;
  Matches  105;  Conservative   96;  Mismatches  218;  Indels  122;  Gaps   23;

Qy         14 RNGIDGHALADRIGLDEAE------IAWRLSFTGIDDDTMAA----------------L 50
              |||:      |:  |: |:      |  : | ||:  |:: |                 :
Db         31 RNGL----TVDKAPLENAKNQLQHSIDTQTSTTGMTQDSINAYNAKLTAARNKIQQINQV 86

Qy         51 AAEQPLFE------ATADALVTDFYDHLESYERTQDLFANSTKTVEQLKE-----TQAEY 99
                | | |      :||:  :|  ||          : ||  ||::     |
Db         87 LAGSPTVEQINTNTSTANQAKSDL-DHARQALTPDKAPLQTAKT--QLEQSINQPTDTTG 143

Qy        100 LLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEE 159
              :       |: :  | | :: :|: ||   | |                    : |:  |
Db        144 MTTASLNAYNQKLQAARQKLTEINQVLNGNPTV----------------QNINDKVTE 185

Qy        160 AAAAVDEL-VARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQ-------ELANAV 211
              |  | |:|  ||      : || |:| |: |         ||   :  |       :  ||
Db        186 ANQAKDQLNTAR-----QGLTLDRQPALTT--------LHGASNLNQAQQNNFTQQINAA 232

Qy        212 ATH-----VEAPLSSLEA---------------TSQDVAERTDTMRARTDDQVDRMADV 250
                |     ::: :::|                : |:  : |   :   |: |:     |
Db        233 QNHAALETIKSNITALNTAMTKLKDSVADNNTIKSDQNYTDATPANKQAYDNAVNAAKGV 292

Qy        251 SREISSVSASVEEVASTADDVRRTSE--DAEALAQQGEAAADDALATMTDIDEATDGVTA 308
                | :: :  |  |    |  |: | :  | :   |: :  | :|:   :|:::|
Db        293 IGETTNPTMDVNTVNQKAASVKSTKDALDGQQNLQRAKTEATNAITHASDLNQAQKN--- 349

Qy        309 GVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADE-VKALAE 367
              : |    | :|::|    :|| : |   :|| ::   : | |      | :|  | |
Db        350 ALTQQVNSAQNVQAV----NDIKQTTQ--SLNTAMTGLKRGVANHNQVVQSDNYVNADTN 403

Qy        368 ESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAAS 427
              :  :  :        :  :    |   :||  :   |  | |:    ::  | ::| :
Db        404 KKNDYNNAYNHANDIINGNAQHPVITPSDVNNAL-SNVTSKEHALNGEAKLNAAKQEANT 462

Qy        428 GMQEVSTATDEQAVSTEEV---AEMVDGVD---DRAGEIAAALDDI--ADATDQQVRTVE 479
              :  ::   : |  : :     |  :| |:     |  : :|: ::  | |   ||:  |
Db        463 ALGHLNNLNNAQRQNLQSQINGAHQIDAVNTIKQNATNLNSAMGNLRQAVADKDQVKRTE 522

Qy        480 E 480
              :
Db        523 D 523


RESULT 11
US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 975
;   LENGTH: 989
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-975

  Query Match             5.9%;  Score 140.5;  DB 1;  Length 989;
  Best Local Similarity   18.6%;  Pred. No. 0.19;
  Matches  113;  Conservative  122;  Mismatches  219;  Indels  153;  Gaps   27;

Qy          5 NDTLVTADVRNGIDGHA-LADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADA 63
              :|:   ||    |   |   | : | :|::|   | |  : :    | |: |  || ||

Db        336 SDSTTGADSLLDISSEADQQDLLSLLQAKVA---SLTLHNKELQDKLQAKSPK-EAEADL 391

Qy         64 LVTDFYDHLESYERTQ-DLFANSTKTVE----QLKETQAEYLLGLGRGEYDTEYAAQRAR 118
                    :||  || ||  :  |  |       | : :  :  ||:   | :       |
Db        392 -------SFDSYHSTQTDLGPSLGKPGETSPPDSKSSPSVLIHSLGKSTTDND-----VR 439

Qy        119 IGKIHDVLGLGPDV------------YLGAYTRYYTGLLDALADDVVADRGEEAAAAVDE 166
              | :: ::|    |:             |    :      |  | :  :::   : :  : |
Db        440 IQQLQEIL---QDLQKRLESSEAERKQLQVELQSRRAELVCLNNTEISENSSDLSQKLKE 496

Qy        167 LVARFLPMLK-LLTFDQQI--------AMDTYIDSYAQRL-HDEID-SRQELANAV---- 211
                :::   :| :|:  :|:         :|| |   :  |:  :||:  :|:| ||:
Db        497 TQSKYEEAMKEVLSVQKQMKLGLVSPESMDNYSHFHELRVTEEEINVLKQDLQNALEESE 556

Qy        212 ------------------ATHVEAPLSSLE-------------------------ATSQD 228
                                 | :: |:   |                         ::
Db        557 RNKEKVRELEEKLVEREKGTVIKPPVEEYEEMKSSYCSVIENMNKEKAFLFEKYQEAQEE 616

Qy        229 VAERTDTMRARTDDQ-----------VDRMAD-VSREISSVSASVEEVASTADDV--RRT 274
              : :  ||::::   :           ::|| | :::::| :|   :|  :  :|   |::
Db        617 IMKLKDTLKSQMTQEASDEAEDMKEAMNRMIDELNKQVSELSQLYKEAQAELEDYRKRKS 676

Qy        275 SEDAEA-------------LAQQGEAAADDALATM-----------TDIDEATDGVTAGV 310
              ||  |             |     | |:|||: |           | : :  |
Db        677 LEDVTAEYIHKAEHEKLMQLTNVSRAKAEDALSEMKSQYSKVLNELTQLKQLVDAQKENS 736

Qy        311 EQLGERAADVESVTGVIDDIAEQTNML---ALNASIEAAR-AGEAGEGFAVVADEVKALA 366
              : |    : ::     :: |: : |      :  :| |:   :  |  | : | :   :
Db        737 VSITEHLQVITTLRTAAKEMEEKISNLKEHLASKEVEVAKLEKQLLEEKAAMTDAMVPRS 796

Qy        367 EESREQSTRVEELVEQMQAETEETVDQLDEVNQ---RIGEGVERVEEAMETLQEITDAVE 423
              : ||: :|  |  : :: :|:| : ::|:    :|   | :|:   | :| :  : |
Db        797 SYEKLQSS-LESEVSVLASKLKESVKEKEKVHSEVVQIRSEVSQVKREKENIQTLLKSKE 855

Qy        424 DAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIAD-ATDQQVRTVEEVR 482
                |||:    :   : ||:|||      |  | :: |::  |   ::  : | :::
Db        856 ------QEVNELLQKFQQAQEELAEM-----KRYAESSSKLEEDKDKKINEMSKEVTKLK 904

Qy        483 ETVGKLS 489
              | :  ||
Db        905 EALNSLS 911


RESULT 12
US-10-821-234-901
; Sequence 901, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 901
;   LENGTH: 1586
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-901

  Query Match             5.8%;  Score 139.5;  DB 1;  Length 1586;
  Best Local Similarity   20.3%;  Pred. No. 0.37;
  Matches   90;  Conservative   72;  Mismatches  183;  Indels   99;  Gaps   15;

Qy         83 ANSTKTVEQLKETQAEYLLGLGR-----GEYDTEYAAQRARIGKIHDVLGLGPDVYLGAY 137
              |  |  :||   : |       |      |: |    : :|  : : |  ||:  |
Db        915 AGEAKVKKQLVAREQEITAVQARMQASYREHVKEVQQLQGKIRTLQEQLENGPNTQLARL 974
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```
Qy        138 TRYYTGLLDAL---ADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYA 194
Db        975 QQENSILRDALNQATSQVESKQNAELAKLRQEL-------------SKVSKELVEKSEA 1020

Qy        195 QRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREI 254
Db       1021 VR---QDEQQRKALEAKAAAFEKQVLQLQASHR---ESEEALQKRLD-------EVSREL 1067

Qy        255 ---SSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVE 311
Db       1068 CHTQSSHASLRADAEKAQEQQQQMAELHSKLQSSEAEVRSKCEELSGLHGQLQEARAENS 1127

Qy        312 QLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESRE 371
Db       1128 QLTERIRSIE------------------ALLEAGQARD--------AQDVQASQAEADQ 1160

Qy        372 QSTRVEELVEQMQA------ETEETVDQ-------LDEVNQRIGEGVERVEEA-METLQE 417
Db       1161 QQTRLKELESQVSGLEKEAIELREAVEQQKVKNNDLREKNWKAMEALATAEQACKEKLHS 1220

Qy        418 ITDAVEDAASGMQEVSTATDE---------QAVSTEEVAEMVDGVDDRAGEI-------A 461
Db       1221 LTQAKEESEKQLCLIEAQTMEALLALLPELSVLAQQNYTEWLQDLKEKGPTLLKHPPAPA 1280

Qy        462 AALDDIADATDQQVRTVEEVRETV 485
Db       1281 EPSSDLA----SKLREAEETQSTL 1300
```

RESULT 13
US-10-793-626-3154
; Sequence 3154, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3154
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3154

Query Match 5.7%; Score 137.5; DB 1; Length 1095;
Best Local Similarity 17.5%; Pred. No. 0.31;
Matches 88; Conservative 91; Mismatches 200; Indels 125; Gaps 16;

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Qy         87 KTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGP-------------DVY 133
Db        160 QAVDQVPST--EGMTQQTKDDYNSKQQAAQQEISKAQQVIDNGDATTQQISNAKTNVERA 217

Qy        134 LGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSY 193
Db        218 LEALNNAKTGLR--------ADK-EELQNAYNQLTQ---------NIDTSGKTPASIRKY 259

Qy        194 AQ---RLHDEIDSRQELANAVATH-------VEAPLSSLEATSQDVAERTDTMRARTDDQ 243
Db        260 NEAKSRIQTQIDSAKNKANSILTNDNPQVSQVTAALNKIKAVQPELDKAIAMLKNKENNN 319

Qy        244 V-----DRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQ----GEA------- 287
Db        320 ALVQAKQQLQQIVNEVDPTQGMTTDTANNYKSKKREAEDEIQKAQQIINNGDATEQQITN 379
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Qy        288 --------------AADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQ 333
Db        380 ETNRVNQAINAINKAKNDLRADKSQLENAYNQLIQNVDTNGKKPASIQQYQAARQAIETQ 439

Qy        334 TNMLALNASIEA--------------ARAGEAGEGFAV-VADEVKAL-----------AE 367
Db        440 YN----NAKSEAHQILENSNPSVNEVAQALQKVEAVQLKVNDAIHMLQNKENNSALVTAK 495

Qy        368 ESREQSTRVEELVEQMQAET-----------------EETVDQLDEVNQRIGEGVERVE 409
Db        496 NQLQQAVNDQPLTTGMTQDSINNYVAKRNEAQSAIRNAEAVINNGDATAKQISDEKSKVE 555

Qy        410 EAMETL----QEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALD 465
Db        556 QALAHLNDAKQQLTADTTELQTAVQQLNRRGDTNNKKPRSINAYNKAIQSLETQITSAKD 615

Qy        466 DIADATDQQVRTVEEVRETVGKLS 489
Db        616 NANAVIQKPIRTVQEVNNALQQVN 639
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RESULT 14
US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match 5.6%; Score 134.5; DB 1; Length 5024;
Best Local Similarity 19.2%; Pred. No. 2.4;
Matches 102; Conservative 94; Mismatches 199; Indels 135; Gaps 22;

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Qy         22 LADRIG---LDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATADALVTDFYDHLESYERT 78
Db        544 IINEIGNPTLNKSEIEQKLQQL---TDAQNALQGSHLLEEAKNNAIT-------EINKLT 593

Qy         79 QDLFANSTKTVEQLKETQ----AEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYL 134
Db        594 ALNDAQRQKAIENVQAQQTIPAVNQQLTLDR-EINTAMQALRDKVGQQNNV--------- 643

Qy        135 GAYTRYYT----------------GLLDALADDVVADRGEEAAAAVDELVARFLPMLKL 177
Db        644 HQQSNYFNEDEQPKHNYDNSVQAGQTIIDKLQDPIM--NKNEIEQAINQINT-------- 693

Qy        178 LTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMR 237
Db        694 ----TQTAL-----SGENKLHTD----QESTN---RQIEG-LSSLN-TAQINAEKDLVNQ 735

Qy        238 ARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTS----------------EDAEA 280
Db        736 AKTRTDVAQKLATAKEINSAMSNLRDGIQNKEDIKRSSAYINADPTKVTAYDQALQNAEN 795

Qy        281 L------AQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQT 334
```

```
                :       :  :|  : ||: :    :  |||        :    |  :  : |    :
Db        796 IINATPNVELNKATIEQALSRVQQAQQDLDGVQQLANAKQQATQTVNGLNSLNDGQKREL 855

Qy        335 NML------------ALNASIEAARAGEAGEGFAVVADEVKA---LAEESREQSTRVEEL 379
              |:|              || : |:  | ||         |:||       | : :    :
Db        856 NLLINSANTRTKVQEELNKATESNHAMEALRNSVQNVDQVKQSNNYVNEDQPEQHNYDNA 915

Qy        380 VEQMQA----ETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTA 435
              | : ||      :  :|:|    :|: : |   ::|:   |::     : | :|:: :::
Db        916 VNEAQATINNNAQPVLDKL--AIERLTQTVNTTKDALHGTQKLIQDQQAAETGIRGLTSL 973

Qy        436 TDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
               : |     |||::                  |  |  :|| : :   |:
Db        974 NEPQ--KNAEVAKVT----------------AATTRDEVRNIRQEATTL 1004


RESULT 15
US-10-821-234-1632
; Sequence 1632, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1632
;   LENGTH: 284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1632

  Query Match             5.6%;  Score 134;  DB 1;  Length 284;
  Best Local Similarity   22.0%;  Pred. No. 0.11;
  Matches   61;  Conservative   57;  Mismatches  135;  Indels   24;  Gaps    8;

Qy        155 DRGEEAAAAVDELVARFLPMLKLLTFDQQI------AMDTYIDSYAQRLHDEIDSRQELA 208
              || |:| |   :   |    | |  :||       :  :: |:: :  |   : | |
Db         20 DRAEQAEADKKQAEDR----CKQLEEEQQALQKKLKGTEDEVEKYSESV-KEAQEKLEQA 74

Qy        209 NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTA 268
              ||  || ::||    | | |  |  : |    : :: :  :        :: : : |
Db         75 EKKATDAEADVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRA 134

Qy        269 DDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVID 328
                |  |   :: :  |:|:     ::       :   :|:  |||   ||    ::
Db        135 MKDEEKMELQEMQLKEAKHIAEDSDRKYEEVARKLVILEGELERSEERAEVAESRARQLE 194

Qy        329 DIAEQTNMLALNASIEAARAGEAGEGFAVVAD----EVKALAEESREQSTRVEELVEQMQ 384
              :       :  :: ::::  | |  | ::   |    |:| | |: :|  ||  |  |:
Db        195 E-----ELRTMDQALKSLMASE--EEYSTKEDKYEEEIKLLEEKLKEAETRA-EFAERSV 246

Qy        385 AETEETVDQLDE-VNQRIGEGVERVEEAMETLQEITD 420
              |: |:|:| |:| :     | ||  :   :|| |: :
Db        247 AKLEKTIDDLEETLASAKEENVEIHQTLDQTLLELNN 283


Search completed: November 23, 2005, 05:09:26
Job time : 17.766 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:37:11 ; Search time 47.9554 Seconds
(without alignments)
843.041 Million cell updates/sec

Title: US-09-455-978B-2
Perfect score: 2394
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....ATDQQVRTVEEVRETVGKLS 489

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	412.5	17.2	640	2	US-09-252-991A-23252	Sequence 23252, A
2	401.5	16.8	545	2	US-09-252-991A-31086	Sequence 31086, A
3	398	16.6	663	2	US-09-252-991A-23255	Sequence 23255, A
4	397.5	16.6	906	2	US-09-252-991A-32715	Sequence 32715, A
5	389.5	16.3	696	2	US-09-252-991A-16965	Sequence 16965, A
6	388.5	16.2	897	2	US-09-902-540-15636	Sequence 15636, A
7	385	16.1	710	2	US-09-252-991A-32789	Sequence 32789, A
8	380.5	15.9	734	2	US-09-252-991A-30703	Sequence 30703, A
9	380.5	15.9	857	2	US-09-252-991A-23956	Sequence 23956, A
10	379	15.8	701	2	US-09-252-991A-23288	Sequence 23288, A
11	373.5	15.6	709	2	US-09-328-352-5172	Sequence 5172, Ap
12	373	15.6	614	2	US-09-252-991A-31412	Sequence 31412, A
13	368.5	15.4	573	2	US-09-252-991A-18744	Sequence 18744, A
14	366	15.3	760	2	US-09-252-991A-31724	Sequence 31724, A
15	361	15.1	613	2	US-09-252-991A-25899	Sequence 25899, A
16	360	15.0	520	2	US-09-902-540-14226	Sequence 14226, A
17	359	15.0	579	2	US-09-543-681A-6665	Sequence 6665, Ap
18	358.5	15.0	611	2	US-09-252-991A-20097	Sequence 20097, A
19	352.5	14.7	563	2	US-09-252-991A-31048	Sequence 31048, A
20	350.5	14.6	521	2	US-09-902-540-11865	Sequence 11865, A
21	349.5	14.6	487	2	US-09-902-540-14739	Sequence 14739, A
22	349	14.6	510	2	US-09-902-540-15074	Sequence 15074, A
23	348.5	14.6	684	2	US-09-252-991A-28604	Sequence 28604, A
24	347	14.5	547	2	US-09-902-540-16229	Sequence 16229, A
25	346.5	14.5	504	2	US-09-252-991A-26180	Sequence 26180, A
26	343.5	14.3	537	2	US-09-252-991A-20929	Sequence 20929, A
27	334.5	14.0	653	2	US-09-252-991A-18264	Sequence 18264, A
28	334	14.0	572	2	US-09-543-681A-8138	Sequence 8138, Ap
29	333	13.9	413	2	US-09-902-540-12315	Sequence 12315, A
30	333	13.9	645	2	US-09-252-991A-16799	Sequence 16799, A
31	331.5	13.8	620	2	US-09-902-540-12224	Sequence 12224, A
32	329.5	13.8	548	2	US-09-252-991A-23147	Sequence 23147, A
33	321.5	13.4	535	2	US-09-543-681A-4593	Sequence 4593, Ap
34	320.5	13.4	670	2	US-09-252-991A-26867	Sequence 26867, A
35	315	13.2	595	2	US-09-543-681A-6908	Sequence 6908, Ap
36	314.5	13.1	559	2	US-09-902-540-11787	Sequence 11787, A
37	313.5	13.1	596	2	US-09-902-540-13814	Sequence 13814, A
38	313	13.1	552	2	US-09-543-681A-8191	Sequence 8191, Ap
39	313	13.1	680	2	US-09-252-991A-26639	Sequence 26639, A
40	301.5	12.6	482	2	US-09-902-540-16520	Sequence 16520, A
41	295	12.3	520	2	US-09-902-540-11891	Sequence 11891, A
42	294	12.3	506	2	US-09-902-540-10933	Sequence 10933, A
43	292.5	12.2	531	2	US-08-976-063E-34	Sequence 34, Appl
44	292.5	12.2	556	2	US-09-902-540-13058	Sequence 13058, A
45	288.5	12.1	449	2	US-09-902-540-13188	Sequence 13188, A

ALIGNMENTS

RESULT 1
US-09-252-991A-23252
; Sequence 23252, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23252
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23252

Query Match 17.2%; Score 412.5; DB 2; Length 640;
Best Local Similarity 24.4%; Pred. No. 1.1e-24;
Matches 149; Conservative 97; Mismatches 199; Indels 165; Gaps 19;

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Qy          7 TLVTADVRNGIDG-----HALADRIGL----DEAEIAWRLSFTGIDDDTMAALAAEQPLF 57
              ||  ::::: ::|       || :: |    ||| || :|               |||:|
Db         59 TLTASNIQSWLEGRMHLVEGLASQLALLDQPDEANIARQL--------------EQPVF 103

Qy         58 ----------EATADALVTDFYDHL-ESYE-RTQDLFANS-------------TKTVEQ 91
                      || :      || : | |: ||:  : ::                 | ||
Db        104 SRNFASVYLGEAASGTFTMRPYDAMPEGYDPRTRAWYKDALAADRLIVTEPFVDAGTGEQ 163

Qy         92 -----LKETQAEYLLGLGRGEYDTE--------------YAAQRARIGKI--HDVLGL- 128
                  |    |  |||:  |:   |                ||  :  |||  |   ||
Db        164 ILAMSLPVRHAGQLLGVAAGDMKLETLTAILNSLKFDGAGYAFLVSDAGKILLHPDSGLV 223

Qy        129 -----------GPDVYLGAY---------------------TRYYTGLLD--------- 146
                        |::  | :                      | |   :||
Db        224 LKTLAEAYPKGAPNIVPGVHEVELDGRSQFVSFTPVKGLPGVTWYVALVLDRDTAYSMLS 283

Qy        147 -----ALADDVVA--------------------DRG---EEAAAAVDELVARFLPMLKLL 178
                  |:   ::|                    | |   :: |    :|  |    ||:
Db        284 EFRTSAIVATLIAVVGIMLLLGMLIRVLMQPLTDMGRAMQDIAQGEGDLTKR----LKVT 339

Qy        179 TFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRA 238
              : |:   :    : : :|:|: |   :|:|                |   :| |   :::  |
Db        340 SNDEFGTLANAFNRFVERIHESI---REVAGTA--------RQLHDVAQLVVNASNSSMA 388
```

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Qy        239 RTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTD 298
Db        389 NSDEQSNRTNSVAAAINELGAAAQEIARNAADASHHASDANHQAEDGKQVVEQTIRAMNE 448

Qy        299 IDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVV 358
Db        449 LSEKISASCANIEALNSRTVNIGQILEVIKGISEQTNLLALNAAIEAARAGEAGRGFAVV 508

Qy        359 ADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEI 418
Db        509 ADEVRNLAHRAQESAQQIQKMIEELQIGAQEAVSTMTESQRYSLESVEIANRAGERLGSV 568

Qy        419 TDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTV 478
Db        569 TSRIGEIDSMNQSVATATEEQTA-------VVDSLNMDITEINTLNQEGVENLQATLRAC 621

Qy        479 EEVRETVGKL 488
Db        622 GELETQAGRL 631
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RESULT 2
US-09-252-991A-31086
; Sequence 31086, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31086
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31086

Query Match 16.8%; Score 401.5; DB 2; Length 545;
Best Local Similarity 24.9%; Pred. No. 6.6e-24;
Matches 131; Conservative 111; Mismatches 205; Indels 79; Gaps 16;

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Qy          3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD 62
Db         47 SENELSVNA-LRNHMEGDMMHD----------------ALRADVLAAFVV-QPGDGAAAE 88

Qy         63 ALVTDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRA 117
Db         89 QVRQDLQEHSQWFR----------KVVEQNQGLPLNDAIHQALVEL-RPDLEAYIGAAES 137

Qy        118 RIGK-IHDVLGLGPDV--YLGAYTRYYTGLLDALADDV-----VADRGEE---------- 159
Db        138 IVGKALLDPVAARAELPQFVQAF-KELEGRNEALSSLIEKHVEQTNRAREDSMRYSAWML 196

Qy        160 ------AAAAVDELVARFL-----PMLKLL---------TFDQQIAMDTYIDSYAQRLHD 199
Db        197 AGGILVACLVLGQLCRQLLRAVLKPLRKLVASARVIAQGNLQEPIGVDS--DDEAGQLQR 254

Qy        200 EIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSA 259
Db        255 ALGEMQENLRQMITIIRQESEELHDTSQSIGQTSQSIVDGASQQADSATSMAASMEEMIT 314

Qy        260 SVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAAD 319
Db        315 NISQISDHADNARVISAKSEELASSGGQVILNVVEGMSRIADVVNQSSTSITALGQSSDE 374

Qy        320 VESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEEL 379
```

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Db        375 IHSIIQVIKGIAEQTNLLALNAAIEAARAGEAGRGFAVVADEVRGLAARTTQSTQEITAM 434

Qy        380 VEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQ 439
Db        435 IERIRASTGQAINSMEAGVSRVNEGVSFARQAGVSINEILDGTRHAASVVDEISQTIREQ 494

Qy        440 AVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
Db        495 SRASDEIAQRVELIAQRSQQNTQAMHEMA-AT---ARRLNEVAATM 536
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RESULT 3
US-09-252-991A-23255
; Sequence 23255, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23255
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23255

Query Match 16.6%; Score 398; DB 2; Length 663;
Best Local Similarity 28.3%; Pred. No. 1.6e-23;
Matches 118; Conservative 74; Mismatches 171; Indels 54; Gaps 10;

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Qy        103 LGRGEYDTEYAAQRARIGKIHDVLGL-GPDVYLG-------AY---TRYYTGLLDALADD 151
Db        261 IGSGFSEAELHG-NTRILSFSPVKGLSGLDWYIGISVDKDKAYAMLTKLRTSAIVAALIA 319

Qy        152 VVA-----------------DRG---EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYID 191
Db        320 VVAIVLLLGMLIRVLMQPLTDMGRAMQDIAQGEGDLTKR----LKVTSNDEFGTLANAFN 375

Qy        192 SYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVS 251
Db        376 RFVERIHESI---REVAGTA--------RQLHDVAQLVVNASNSSMANSDEQSNRTNSVA 424

Qy        252 REISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVE 311
Db        425 AAINELGAAAQEIARNAADASHHASDANHQAEDGKQVVEQTIRAMNELSEKISASCANIE 484

Qy        312 QLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESRE 371
Db        485 ALNSRTVNIGQILEVIKGISEQTNLLALNAAIEAARAGEAGRGFAVVADEVRNLAHRAQE 544

Qy        372 QSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQE 431
Db        545 SAQQIQKMIEELQIGAQEAVSTMTESQRYSLESVEIANRAGERLSSVTGRIAEIDGMNQS 604

Qy        432 VSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKL 488
Db        605 VATATEEQTA-------VVDSLNMDITEINTLNQEGVENLQATLRACGELETQAGRL 654
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RESULT 4
US-09-252-991A-32715
; Sequence 32715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 32715
;   LENGTH: 906
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32715

  Query Match             16.6%;  Score 397.5;  DB 2;  Length 906;
  Best Local Similarity   24.8%;  Pred. No. 2.8e-23;
  Matches  129;  Conservative   87;  Mismatches  158;  Indels  147;  Gaps   13;

Qy          79 QDLFANSTKTVEQLK-------ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPD 131
Db         406 QDLFNNRMKPISQLKIVADAVAVSVVDALHKYRAGVFDEERLQQELS------------- 452

Qy         132 VYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLL------------- 178
Db         453 ---GALSRIEKSWADYSAD--------HRTAAEKEIIESLVPTLERVKRMTLAYGEQARA 501

Qy         179 ---------TFDQQI---------AMDTYID---SYAQRLHDEIDSRQE----------- 206
Db         502 GSLRNVEAGTFNREMYGAFDPLGTALSTLIDLQLSEGAKLNEQMEKRYDSMRTTFLLIGA 561

Qy         207 --------LANAVATHVEAPLSSLEATSQDVAERTD-TMR--ARTDDQV----------- 244
Db         562 AALVLIVAAAWFISLSIMRPLSDLRGVIRRVQDSSNLTLRADARGRDEVSDTARAFNMML 621

Qy         245 ---------------------DRMADVSREISSVSAS-----------VEEVASTADDVR 272
Db         622 ESQQALLRHLAETARKLTITSDEMSAISNQVSHVATSQGDQTDMVATAVHQMSMAVQDVA 681

Qy         273 RTSEDAEALAQQGEAAADDALATMTDIDEATDGVT-------AGVEQLGERAADVESVTG 325
Db         682 RNAQAAAASAESANSEAHTGTGLVHANLDAIQGLSVMVGEAGAVIDTLRNKTEEISTVLE 741

Qy         326 VIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQA 385
Db         742 VIQNIAQQTNLLALNAAIEAARAGEAGRGFAVVADEVRSLATNTHKATETIREMIEALQA 801

Qy         386 ETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEE 445
Db         802 GASSAVSVMQQSREQAQVSVQRAHEAGKALGLIAQAVEGIAQSNAQISTATEEQTATASE 861

Qy         446 VAEMVDGVDDRAGEIA----------AALDDIADATDQQVR 476
Db         862 VSQNIDSLNASIGEVAEGAVKTSTSSVELAKLANGLEQQIQ 902


RESULT 5
US-09-252-991A-16965
; Sequence 16965, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16965
;   LENGTH: 696
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16965

  Query Match             16.3%;  Score 389.5;  DB 2;  Length 696;
  Best Local Similarity   25.3%;  Pred. No. 8.4e-23;
  Matches  131;  Conservative   98;  Mismatches  210;  Indels   79;  Gaps   14;

Qy           1 MSNDNDTLVTADVRNGIDGHALADRI--GLDEAEIAWRLSFTGIDDDTMAALAAEQPLFE 58
Db         213 LAGDENSVQAAD-SFGRDA-SLFGRVLKGMQEGNAAMSISKV-TNAEAVDRLNEIAELFE 269

Qy          59 ATADALVTDFYDHLESYERTQDLF-----ANSTKTVEQLKETQAEYLL----GLGRGEYD 109
Db         270 -----FVSGSVD--EILETSPDLFQVREAANNIFSVSQTLLDKASQLADGFENLAGGRSI 322

Qy         110 TEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTG-----------------LLDALAD 150
Db         323 NLFA------GYVLGALALASIILIGLVMVRETNRRLAETAEKNDRNQAAILRLLDEIAD 376

Qy         151 DVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELA-- 208
Db         377 --LADGDLTVAATVTE--------------------DFTGAIADSINYSIDQLRELVET 413

Qy         209 -NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVAST 267
Db         414 INQTAVQVAAAAQETQSTAMHLAE-------ASEHQAQEIAGASAAINEMAVSIDQVSAN 466

Qy         268 ADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVI 327
Db         467 ASESSAVAERSVAIANKGNEVVHNTITGMDNIREQIQDTSKRIKRLGESSQEIGDIVSLI 526

Qy         328 DDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAET 387
Db         527 NDIADQTNILALNAAIQASMAGDAGRGFAVVADEVQRLAERSSAATKQIEALVKTIQTDT 586

Qy         388 EETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVA 447
Db         587 NEAVISMEQTTSEVVRGARLAQDAGVALEEIEKVSKTLAALIQNISNAARQQASSAGHIS 646

Qy         448 EMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
Db         647 NTMNVIQEITSQTSAGTTATARSIGNLAKMASEMRNSV 684


RESULT 6
US-09-902-540-15636
; Sequence 15636, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15636
;   LENGTH: 897
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-15636

  Query Match             16.2%;  Score 388.5;  DB 2;  Length 897;
  Best Local Similarity   26.1%;  Pred. No. 1.4e-22;
  Matches  132;  Conservative  107;  Mismatches  202;  Indels   65;  Gaps   15;

Qy           2 SNDNDTLVTADVRNGIDGHAL--ADRIGLD----EAEIAWRLSF-TGIDDDTMAALAAEQ 54
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Db        340 NGDRSVARSVTLSGGVVGQALLVLDNSGLDAVVTELQRVVMLAFGIGLTLFLLVAFFISR 399

Qy         55 PLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAA 114

Db        400 AFILVPLDAMM-GMARRLAEADLTGRVDVGTRDELGQL----AEALNRIAQSWRDT---- 450

Qy        115 QRARIGKIHDVLGLGPDVYLGAYTRYY-TGLLDALADDVVADRGEEAAAAVDELVARFLP 173

Db        451 ----LGRVRGV----SDVVAGVVEQIHRTGTTVSSGAGTVQARVEETSSSMVEMMASL-- 500

Qy        174 MLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELA---NAVATHVEAPLSSLEATSQDVA 230

Db        501 --------RGIAEN--VEVLYQSAEESSSSIMEMAATNDEVAENVQAMAASVEETTSAIE 550

Qy        231 ERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADD----VRRTSEDAEALAQQGE 286

Db        551 EMTFSIK-----------EVATNIQELSASTEETSSAISQMDAAIGQVEANAKETARLSE 599

Qy        287 AAADDALA-------TMTDID---EATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNM 336

Db        600 QVFDDAQTGVESLRKTLTGIDRIKETSRSAAHVIESLGRRISEIGNILNVIDDVAEQTNL 659

Qy        337 LALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDE 396

Db        660 LALNAAIIAAQAGEHGKGFAVVAEEIKDLAERTGASTKEIAELIRSIQEESRNAVVVMNQ 719

Qy        397 VNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDR 456

Db        720 GVRSVEEGVQLGREAEGALRKINDSTQKSTQMVKAIARATVEQARGSKQVTASIHRISET 779

Qy        457 AGEIAAALDDIADATDQQVRTVEEVR 482

Db        780 VQQISKASNEQARGGEQIMKSAEKMK 805


RESULT 7
US-09-252-991A-32789
; Sequence 32789, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 32789
;   LENGTH: 710
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32789

  Query Match             16.1%;  Score 385;  DB 2;  Length 710;
  Best Local Similarity   27.8%;  Pred. No. 2e-22;
  Matches  131;  Conservative   83;  Mismatches  215;  Indels   42;  Gaps   10;

Qy         39 FTGIDDDTMAALAAEQPLFEAT----------ADALVTDFYDHLESYERTQDLFANS--- 85

Db        257 FERSDKAEQAAFAAFDALRQAATTLRGQLPGEADAALEQAMGSLQGYRGGIEQFRAGVIR 316

Qy         86 TKTVEQLKETQAEYLLGLGR-----GEYDTEYAAQRARIGK-IHDVLGLGPDVYLG-AYT 138

Db        317 TRQAQQAMQSSTQDMARAGRTLTEAGRQLRESTASRDRASLWLIAALALAFGCVAGWAIN 376

Qy        139 RYYTGLLD-ALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRL 197

Db        377 RQIVRPLDEALA--------QAEAIAAGDLGKRPQNPLTLQRRDEL--------GQLQRV 420

Qy        198 HDEI-DSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISS 256

Db        421 MQRMGDSLRELVGRIGDGV----SQLASSAEELSAVTEQTRAGVNSQKVETDQVATAMHE 476

Qy        257 VSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316

Db        477 MAATVQDVARNAELASQAARQADEEARQGDAVVDQAVTRIERLASEMDVSSEAMARLKNE 536

Qy        317 AADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRV 376

Db        537 SEQIGSVLDVIKSVAEQTNLLALNAAIEAARAGDAGRGFAVVADEVRGLAQRTQQSTAEI 596

Qy        377 EELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436

Db        597 EGLIQRLQQGAGEAAERLENSRSLTASTVELARRAGAALDSITRTVSDIQNMNLQIATAA 656

Qy        437 DEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGK 487

Db        657 EQQSTVAEEINRSVLSVRDVAEQSAAASEQTAASSGELARLGTQLQAQVGR 707


RESULT 8
US-09-252-991A-30703
; Sequence 30703, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 30703
;   LENGTH: 734
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30703

  Query Match             15.9%;  Score 380.5;  DB 2;  Length 734;
  Best Local Similarity   24.7%;  Pred. No. 4.7e-22;
  Matches  119;  Conservative   91;  Mismatches  178;  Indels   93;  Gaps   13;

Qy         41 GIDDDTMAALAAEQPLFEATADALVTDFYDHLESY----------ERTQDLFANSTKTVE 90

Db        310 GNEVDNLKNLTVDQPLYDIDAE------HGHIELFLPFTIADSGVRWTLMLQIPQAAVFG 363

Qy         91 QLKETQAEY-------LLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAY-----T 138

Db        364 ELQQLQGELSDQRQQDILGM-------------SLAGLVVAALGL-LVVWLVGYGIARPL 409

Qy        139 RYYTGLLDALAD---DVVADRGEEAAAAVDEL--VARFLPMLKLLTFDQQIAMDTYIDSY 193

Db        410 RQLVGMLDDIAQGEGDLTRRLSSERA---DELGSIAK-------------GFNTFLGKL 452

Qy        194 AQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSRE 253

Db        453 QNMIGQVVQSVQKVS------------------DSSEHTADIAIRTNQGVQQQL---AE 490

Qy        254 ISSVSASVEEVASTADDVRR-------TSEDAEALAQQGEAAADDALATMTDIDEATDGV 306

Db        491 IELVATAVHEMTATAQDVARNATHAAEAANHADQAAHQGKQIVESSSAAIQALASEIGRA 550

Qy        307 TAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALA 366

Db        551 VGVVQNLAKDSENINAILVAIRGIAEQTNLLALNAAIEAARAGEQGRGFAVVADEVRNLA 610

Qy        367 EESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAA 426
```

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              ::::: :  :: :::|:|  | : |  : :  :|  : |    :| | |: || ||
Db        611 QKTQQATEEIQSMIQQLQQGTRDVVKVMQDSQERTDDSVRHARQAAEALESITQAVSVIN 670

Qy        427 SGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVG 486
                ::::| :||:   |::   |  :   | ::|   |: : |: :  |  |: |  |
Db        671 DMNPQIASAAEEQSAVAEDINRNVANIGQVANQVAGGADEASQASAELTRLAEQQRRLVN 730

Qy        487 K 487
                :
Db        731 Q 731


RESULT 9
US-09-252-991A-23956
; Sequence 23956, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 23956
;   LENGTH: 857
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23956

  Query Match             15.9%;  Score 380.5;  DB 2;  Length 857;
  Best Local Similarity   26.8%;  Pred. No. 5.9e-22;
  Matches  141;  Conservative   92;  Mismatches  226;  Indels   67;  Gaps   16;

Qy          2 SNDNDTLVTADVRNGIDGHALADRIGLD-------EAEIAW--RLSFTGIDD-----DTM 47
              :|  | | ::   :|   :|| :  | |         |::|   ||   |:|:     :
Db        352 ANSLDILQSSLAEDG--AYALKESQGHDGEPLLQQAAQVAQVNRLVLQGLDEARSRLEAR 409

Qy         48 AALAAEQP---LFEA-----------TADALVTDFYDHLESYERTQDLFANSTKTVEQLK 93
              || | | |   | ||           | || |:   | | :     |  |       ||:
Db        410 AADAQEGPPKSLREALELAARLEQAITDDAYVSVVKDVLTNIRGFADKLAE--YRASQLQ 467

Qy         94 ETQAEYLLGLGRGE----YDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALA 149
              | |    :|   |:     |  : ||:  :  :|  |      : :||        :|  |
Db        468 ERQMYAAMGERAGQVMARVDRSWEAQQQAM--LHS-LRTNSLLIVGA------AVLALLV 518

Qy        150 DDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIA---MDTYIDSYAQRLHDEIDSRQE 206
                  |  ||  :  |: | |: : :   :||  :   :||      ||:
Db        519 -------GLGAAFGISLLIVR--PLRQAMGVAHRIAEGDLAVRVDS---ERRDEVGQLMA 566

Qy        207 LANAVATHVEAPLSSLE-------ATSQDVAERTDTMRARTDDQVDRMADVSREISSVSA 259
                |:   :   :| |:          |: ::  |   |   | |       |:  :: ::|
Db        567 AMRAMTGSLRGIVSQLQDGVGRIAGASEALSGVTTRTRLGIDSQRAETEQVATAMNQMAA 626

Qy        260 SVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAAD 319
              :| |||  |::    :| |:       |:       |  :  : ||    || || |   :
Db        627 TVHEVAHNAEEAAGAAESADGKVSVGQEVVRQTLERIERLAEAVRAATASVEALSADSQR 686

Qy        320 VESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEEL 379
              : ||  ||  :|||||:|||||:|||||||: | ||||||||||:|||  ::: :  :| |
Db        687 IGSVLDVIKSVAEQTNLLALNAAIEAARAGDQGRGFAVVADEVRALARRTQQSTAEIETL 746

Qy        380 VEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQ 439
              :  :|  |:: | ::   :| : : |:   :    |  |  ||       |::: |:::|
Db        747 IGALQNGTQQAVQRMQRSHQLVDQSVDDALQTEAALGNIATAVALIQQMNQQIAAASEQQ 806

Qy        440 AVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
              :   ||:   |  : : | : | |:   | :::|      |::  |
Db        807 SAVAEEINRSVTAIREVADQSAQAMQSTASSSEQLAELGRELQGMV 852


RESULT 10
US-09-252-991A-23288
; Sequence 23288, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 23288
;   LENGTH: 701
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23288

  Query Match             15.8%;  Score 379;  DB 2;  Length 701;
  Best Local Similarity   29.0%;  Pred. No. 5.9e-22;
  Matches   96;  Conservative   67;  Mismatches  146;  Indels   22;  Gaps    4;

Qy        158 EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEA 217
              :: |    :|  |    | : : |:   :    : : :|:|  |   :|:|
Db        384 QDIAQGEGDLTKR----LAVTSRDEFGVLGDAFNQFVERIHRSI---REVAGTA------ 430

Qy        218 PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSED 277
                  |   || |   :::  | :|:| :|   |:  |: : |: :|:|  | |    : |
Db        431 --HKLHDVSQLVVNASNSSMANSDEQSNRTNSVAAAINELGAAAQEIARNAADASHHASD 488

Qy        278 AEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNML 337
              |   |: |:   :  :  | :: |       | :| |  |  ::  :  ||  |:||||:|
Db        489 ANHQAEDGKQVVEQTIRAMNELSEKISASCANIEALNSRTVNIGQILEVIKGISEQTNLL 548

Qy        338 ALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEV 397
              ||||:||||||||| |||||||||: ||  ::| : :::::|::|    | |  : |
Db        549 ALNAAIEAARAGEAGRGFAVVADEVRNLAHRAQESAQQIQKMIEELQVGAREAVATMTES 608

Qy        398 NQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRA 457
              :   | ||    | |:|  :|  : :     | |:|||:||         :|| ::
Db        609 QRYSLESVEIANRAGESLSSVTRRIGEIDGMNQSVATATEEQTA-------VVDSLNMDI 661

Qy        458 GEIAAALDDIADATDQQVRTVEEVRETVGKL 488
              ||     :  :     :|   |:    |:|
Db        662 TEINTLNQEGVENLQATLRACGELETQAGRL 692


RESULT 11
US-09-328-352-5172
; Sequence 5172, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5172
;   LENGTH: 709
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-5172

  Query Match             15.6%;  Score 373.5;  DB 2;  Length 709;
  Best Local Similarity   28.7%;  Pred. No. 1.6e-21;
```

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  Matches  100;  Conservative   67;  Mismatches  141;  Indels   41;  Gaps    5;

Qy        144 LLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS 203
              ||| :|| :|| : | | | :                  :  : |  ::  ||
Db        388 LLDEIAD--LADGDLRSYATVSE--------------------DFTGAIADSINFAIDQ 424

Qy        204 RQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEE 263
              ::|           :| :  |||:||  |   :: |:   :     ::||:  | :: |
Db        425 LRDL----------VSRIHETSQEVARYTQDTQSITNQLAEASEHQAQEIAGASTAMNE 473

Qy        264 VASTADDV-RRTSEDAEA------LAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316
              :| : | |    || ||       :|  |    : ::  | | |     :  :::|||
Db        474 MAQSIDQVSANASESAEVAQRSVQIASNGAQVVNRSIEGMDTIREQIQETSKRIKRLGES 533

Qy        317 AADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRV 376
              : :: ::  :|:|||:|||:|||||:|:|: ||||| |||||||||: ||| |   : ::
Db        534 SQEIGNIVSLINDIADQTNILALNAAIQASMAGEAGRGFAVVADEVQRLAERSASATKQI 593

Qy        377 EELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436
              | ||: :| :| | |  :::   :  |    ::|   | ||     | |  :  :| |
Db        594 ETLVKTIQTDTNEAVISMEQTTTEVVRGANLAKDAGIALDEIQKVSGDLAKLIASISDAA 653

Qy        437 DEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
              |: |   :|  :  | :   :   |  | | :  :     | :||:|
Db        654 KLQSASASHIATTMTVVQEITSQTTTATFDTARSVSELANMAESLRESV 702


RESULT 12
US-09-252-991A-31412
; Sequence 31412, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 31412
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31412

  Query Match             15.6%;  Score 373;  DB 2;  Length 614;
  Best Local Similarity   26.6%;  Pred. No. 1.5e-21;
  Matches  142;  Conservative   87;  Mismatches  214;  Indels   90;  Gaps   18;

Qy          9 VTADVRNGIDGHALADRIG--------LDEAEIAWRLSFTG-IDDDTMAALAAEQPLFEA 59
              :| |||       |  : :|        :|||     | | | : :     |   |
Db        108 LTGDVR------AYRELLGGPVRAAQLIDEA----NLQFRGQVQEWKNVLLRGRQ----- 152

Qy         60 TADALVTDFYDHLESYER-TQDLFANSTKTVEQLKETQAEYLLGLGRGEY---DTEYAAQ 115
               |:|  | ::   |: ||  ||:        |   : : | |    | |:    | |
Db        153 -AEA-QTKYWSQFEAQERAVQDILGRLGSVAEGELKDRVERL----REEHRRLGTAYRQG 206

Qy        116 RARIGKIHDVLGLGPDVYLG-----AYTRYYTGLLDALADDV-------------VADR- 156
              | |       |  | |  |         |  |  : || |::              | |
Db        207 RQRF------LEAGADPIAGDQAVTGIDRATTAQMQALRDELHQASDLHSSSISAEARRT 260

Qy        157 ---------GEEAAAAVDE--LVARFL--PMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS 203
                      |   | |:    || | |  |: :|:    |::   : :    |  ||:
Db        261 MLLGSLVLIGASLAVALLSLWLVNRNLVRPVQRLIEHIAQLSHGDFGERIEIRRKDELGK 320

Qy        204 RQELANAVATHVEAPLSSLEATSQDVAERTDT-------MRARTDDQVDRMADVSREISS 256
                  || :   :       |  :::|:   : :       | | | :|  |   |:  :
Db        321 LALAANTLRDFLVDIFDRLRRSTRDLDSASGSLNAIASLMAAGTREQFSRTDQVATAMQE 380

Qy        257 VSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGER 316
              :||: :|||  | |  | :::|:  ||:||   :: : :: :: :  |      : ||
Db        381 MSATAQEVARYAGDAARAADEADDSAQRGEDVMEETIRSIGEMRKEIDHTVEVIRQLESD 440

Qy        317 AADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRV 376
              :  :  |  ||  ||||||:|||||:|||||||:|| |||||||||: ||: : |    :
Db        441 SGRIGKVLDVIRGIAEQTNLLALNAAIEAARAGDAGRGFAVVADEVRTLAQRTAESIAEI 500

Qy        377 EELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTAT 436
              :::: :|          ::     |   | |:|  |    |::|| :||      :::||
Db        501 HQIIDTVQNGAVNAARAIESGQSRSEAGAEQVANAGAMLRQITASVESIRDMNRQIATAA 560

Qy        437 DEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKLS 489
              :||    |::: :        |||:    || :  :||   |     :  ||
Db        561 EEQTAVAEDISRNLT-------EIAS----IASSNQEQVEQTEAASRDLHGLS 602


RESULT 13
US-09-252-991A-18744
; Sequence 18744, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 18744
;   LENGTH: 573
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18744

  Query Match             15.4%;  Score 368.5;  DB 2;  Length 573;
  Best Local Similarity   25.0%;  Pred. No. 3.1e-21;
  Matches  129;  Conservative   89;  Mismatches  175;  Indels  123;  Gaps   15;

Qy         14 RNGIDGHALADRI-GL--DEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD-ALVTDFY 69
              |: ::||  |::| ||  | ||   :         | :   || ||      |: | | :|
Db        100 RSLLEGHLSAEQIAGLRNDHAENLQQAL------DRVRQYAAMQP---GEAELAKVAEF- 149

Qy         70 DHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLG 129
                 ||   |:: ::  |  |  :           |  |: | :: | |  | ::
Db        150 ------ERGYALWSATSARVLSLAASDPSAAAQLSYGDSDRQFGAMREVINQL------- 196

Qy        130 PDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFL------PMLKLLTFDQQ 183
                                      |  |||||| |   :  |          : |: |
Db        197 ------------------------DEMEEAAAAADGEASSALGERHRWQQVALVAFGLL 231

Qy        184 IAMDTY----------IDSYAQRLHD-----------EIDSRQE------LANAVATHV 215
              : :              :    |||  :             |: || |        ||    :
Db        232 VCLSLVLVFPGLVTRPLQRLLQRLEEIANGDGDLRVRLEVTSRDEPGRLGSAFNAFLDKL 291

Qy        216 EAPLSSLEATSQDVAERTDTMRARTDDQVDRMAD--------VSREISSVSASVEEVAST 267
              :  :  :  : :||:   ::   |   ||: :          ||   : :|::| |||
Db        292 QPLIREVGRVTGEVADSAGSLAGMTAAN-DRLINSEHASVDQVSTAATQMSSAVHEVARN 350

Qy        268 ADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVI 327
              |    : ::||   |::|    :  :  :  :  :  :  ::|| :  | :::|  ||
Db        351 AQSAAQVADDARRQAREGANVVEATIEVIRQLAQEVESSSESIQQLAQETASIDAVLTVI 410

Qy        328 DDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAET 387
              ||||||:|||||:|||||||| | ||||||||||:|||  ::: :  ::  :|::||
Db        411 KGIAEQTNLLALNAAIEAARAGEQGRGFAVVADEVRALAARTQDSTKDIQARIERLQAGV 470

Qy        388 EETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVA 447
              :  |  :  : :  : |||                  |:|:  |  ||
```

```
Db        471 QNAVRAMQSGSLKARDSVER-----------------AAGVDGVLAAT----------G 502

Qy        448 EMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRE 483
              : |  ::| | :||:| :: :   |:  | : ||||
Db        503 DAVGRINDLAAQIASACEEQSRVIDEIARNISEVRE 538


RESULT 14
US-09-252-991A-31724
; Sequence 31724, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 31724
;   LENGTH: 760
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31724

  Query Match           15.3%;  Score 366;  DB 2;  Length 760;
  Best Local Similarity   31.7%;  Pred. No. 7.2e-21;
  Matches   97;  Conservative   61;  Mismatches  126;  Indels   22;  Gaps    4;

Qy        195 QRL-HDEIDSRQELA---NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADV 250
              ||| |   |   |||   |     ::  :  :: : :|     |   | :      |
Db        454 QRLPHTGRDELGELAGWFNRFLDKLQPIIRDVKVSVRDARSTADQSAAISSQTSAGMQQQ 513

Qy        251 SREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAG- 309
              |||  |: :  |: :|| || |::  |   |:  : |  | || :    :: | : |
Db        514 FREIDQVATASHEMTATAQDVARSAAQAADAARGADQATRDGLALIDRTTQSIDSLAANL 573

Qy        310 ------VEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVK 363
                   ||||   : :: ||  ||  ||||||:|||||:|||||||:|| |||||||||:
Db        574 TSAMGQVEQLASSSEEIGSVLEVIRAIAEQTNLLALNAAIEAARAGDAGRGFAVVADEVR 633

Qy        364 ALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVE 423
              ||  :::   ::  ::| :|  | : || :   :::    ||:|:||:  || | :||
Db        634 NLARRTQDSVEQIRGVIEGLQQGTRDVVDAMHGSHRQAQGSVEQVDEAVAALQRIGEAVT 693

Qy        424 DAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRE 483
                  ::::| :||:   ||:   |           ||: |: ::   |     :| :
Db        694 VINDMNLQIASAAEEQSSVAEEINRNV----------AAIRDVTESLSSQAEESAQVSQ 742

Qy        484 TVGKLS 489
              :: :|:
Db        743 SLNRLA 748


RESULT 15
US-09-252-991A-25899
; Sequence 25899, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 25899
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25899

  Query Match           15.1%;  Score 361;  DB 2;  Length 613;
  Best Local Similarity   26.9%;  Pred. No. 1.3e-20;
  Matches  129;  Conservative   75;  Mismatches  204;  Indels   72;  Gaps   11;

Qy         19 GHALADRIGLDEAEIAWRLSFTGIDD-----------------DTMAALAAEQPLFEA- 59
              | | || |       |::   :| |:                  |:  ::  :|| |
Db        164 GKELTDREG------AYQRLISGADERSIYERYLATRQTLLQSQQTLVQMSRSKPLEETR 217

Qy         60 --TADALVTDFYDHLESYERTQD----LFANSTKTVEQLKETQAEYLLGLGRGEYDTEYA 113
                 |    |     |: |  ||      |   : |   |   |  |           ||: :|
Db        218 QYTESTL-------LDQYRATQQQLQALIDFNVKGASQASHTADEV--------YDSAFA 262

Qy        114 AQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLP 173
              |    || :  | ||   |    :|| |  :            ||  |  | |::|
Db        263 AV---IGVLL-VAGLATVVLAWLFTRSITQPI-----------GE--ALRVAEVIA---- 301

Qy        174 MLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERT 233
                  : |    :||       :|   :   |         : :  : | : :::::  |
Db        302 -----SGDLTSRIDTSGRDEPAKLLVALQGMQAQLRQTIQQIGSSATQLASAAEELSAVT 356

Qy        234 DTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDAL 293
              :       | | :   :  :: ::|:|||||  |      |  :|  || |     : :
Db        357 EQGNRSLTQQNDEIQMAATAVNEMTAAVEEVARNASSTSDASSASEQSAQNGRQRVLETV 416

Qy        294 ATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGE 353
              :  : | |  :| |  | |:| |:  |  ||  ||||||:|||||:||||||| | .
Db        417 QAIRLMSEEVDNTSALVGGLAEKAQDISKVLDVIRGIAEQTNLLALNAAIEAARAGEQGR 476

Qy        354 GFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAME 413
              |||||||||:|||  ::| :  :|:::  :|  |   |  :|  : |    :|  | |
Db        477 GFAVVADEVRALAHRTQESTREIEQMIANIQEGTGAAVGAMDSSSVRARNMLEIAEAAGL 536

Qy        414 TLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQ 473
              | || : |          :::|:::||    ||   :  : | : : :|  :  | |: :
Db        537 ALNEIAERVGQINERTLVIASASEQQAQVAREVDRNLVNIRDISLQTSAGSNQTAAASQE 596


Search completed: November 23, 2005, 04:51:19
Job time : 52.9554 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 23, 2005, 04:50:03 ; Search time 159.851 Seconds
(without alignments)
1278.178 Million cell updates/sec

Title: US-09-455-978B-2
Perfect score: 2394
Sequence: 1 MSNDNDTLVTADVRNGIDGH.....ATDQQVRTVEEVRETVGKLS 489

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	399.5	16.7	535	4	US-10-282-122A-66393	Sequence 66393, A
2	399.5	16.7	535	4	US-10-389-647-531	Sequence 531, App
3	386.5	16.1	682	4	US-10-282-122A-66174	Sequence 66174, A
4	374.5	15.6	680	4	US-10-282-122A-69670	Sequence 69670, A
5	371.5	15.5	686	4	US-10-282-122A-68162	Sequence 68162, A
6	361	15.1	644	4	US-10-282-122A-77591	Sequence 77591, A
7	359.5	15.0	891	3	US-09-272-809-5	Sequence 5, Appli
8	356.5	14.9	539	4	US-10-282-122A-51025	Sequence 51025, A
9	348.5	14.6	679	4	US-10-389-647-372	Sequence 372, App
10	348	14.5	626	4	US-10-282-122A-77066	Sequence 77066, A
11	338	14.1	686	4	US-10-282-122A-52305	Sequence 52305, A
12	332	13.9	547	4	US-10-332-288-28	Sequence 28, Appl
13	326	13.6	641	4	US-10-282-122A-77278	Sequence 77278, A
14	315	13.2	643	4	US-10-282-122A-77602	Sequence 77602, A
15	314.5	13.1	501	4	US-10-282-122A-69564	Sequence 69564, A
16	313.5	13.1	541	4	US-10-282-122A-77047	Sequence 77047, A
17	308	12.9	845	4	US-10-282-122A-76517	Sequence 76517, A
18	297.5	12.4	1137	5	US-10-450-763-54582	Sequence 54582, A
19	292.5	12.2	531	2	US-08-976-063C-34	Sequence 34, Appl
20	292.5	12.2	531	3	US-09-750-986D-34	Sequence 34, Appl
21	292	12.2	564	4	US-10-335-977-6156	Sequence 6156, Ap
22	289	12.1	564	4	US-10-335-977-6157	Sequence 6157, Ap
23	289	12.1	565	3	US-09-882-227-462	Sequence 462, App
24	284	11.9	630	3	US-09-882-227-460	Sequence 460, App
25	280	11.7	675	4	US-10-335-977-4944	Sequence 4944, Ap
26	276	11.5	293	4	US-10-335-977-4942	Sequence 4942, Ap
27	273.5	11.4	664	4	US-10-335-977-4943	Sequence 4943, Ap
28	269	11.2	723	5	US-10-994-726-246	Sequence 246, App
29	269	11.2	753	4	US-10-282-122A-47230	Sequence 47230, A
30	269	11.2	753	5	US-10-994-726-245	Sequence 245, App
31	266	11.1	606	5	US-10-994-726-50	Sequence 50, Appl
32	266	11.1	633	5	US-10-994-726-49	Sequence 49, Appl
33	263	11.0	431	4	US-10-389-647-451	Sequence 451, App
34	257	10.7	431	4	US-10-012-819-228	Sequence 228, App
35	254	10.6	433	2	US-08-945-038-6	Sequence 6, Appli
36	252.5	10.5	433	4	US-10-335-977-8500	Sequence 8500, Ap
37	252.5	10.5	438	4	US-10-335-977-8501	Sequence 8501, Ap
38	249.5	10.4	701	5	US-10-450-763-55498	Sequence 55498, A
39	245	10.2	883	4	US-10-369-493-18563	Sequence 18563, A
40	242.5	10.1	191	5	US-10-450-763-48577	Sequence 48577, A
41	241	10.1	654	4	US-10-282-122A-76558	Sequence 76558, A
42	241	10.1	673	4	US-10-335-977-6249	Sequence 6249, Ap
43	239.5	10.0	2310	3	US-09-874-923-120	Sequence 120, App
44	239.5	10.0	2310	3	US-09-991-496-120	Sequence 120, App
45	239.5	10.0	2310	3	US-09-820-843A-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-10-282-122A-66393
; Sequence 66393, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66393
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66393

Query Match 16.7%; Score 399.5; DB 4; Length 535;
Best Local Similarity 25.2%; Pred. No. 1.6e-15;
Matches 132; Conservative 111; Mismatches 206; Indels 75; Gaps 16;

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Qy          3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD 62
              ::|:  | | :|| ::|  : |                :  | :||   ||   | |:
Db         37 SENELSVNA-LRNHMEGDMMHD---------------ALRADVLAAFVV-QPGDGAAAE 78

Qy         63 ALVTDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRA 117
               :  |  :| : :           | |||     | :   : |: | | : :    | :
Db         79 QVRQDLQEHSQWFR----------KVVEQNQGLPLNDAIHQALVEL-RPDLEAYIGAAES 127

Qy        118 RIGK-IHDVLGLGPDV--YLGAYTRYYTGLLDALADDV-----VADRGEE---------- 159
              :|| : | :    ::  :: |: :   |  :||:  :       :|  |
Db        128 IVGKALLDPVAARAELPQFVQAF-KELEGRNEALSSLIEKHVEQTNRAREDSMRYSAWML 186

Qy        160 ------AAAAVDELVARFL-----PMLKLLTFDQQIAMDTY-----IDS--YAQRLHDEI 201
                   |   : :|  : |     |: ||::  : ||         :||   | :|   :
Db        187 AGGILVACLVLGQLCRQLLRAVLQPLRKLVSSARVIAQGNLQEPIGVDSNDEAGQLQRAL 246

Qy        202 DSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASV 261
                ||    : | :      |  ||| : : : ::      | |    ::  :  :  ::
Db        247 GEMQENLRQMITIIRQESEELHDTSQSIGQTSQSIVHGASQQADSATSMAASMEEMITNI 306

Qy        262 EEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVE 321
              :::  ||: |  |  :| || |     : :  |: | :  :  :  :  ||: : ::
Db        307 SQISDHADNARVISAKSEELASSGGQVILNVVEGMSRIADVVNQSSTSITALGQSSDEIH 366

Qy        322 SVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVE 381
              |:  ||  ||||||:|||||:|||||||||| |||||||||: ||  : : :  : ::|
Db        367 SIIQVIKGIAEQTNLLALNAAIEAARAGEAGRGFAVVADEVRGLAARTTQSTQEITAMIE 426

Qy        382 QMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAV 441
              :::| | : :: ::    |: |||    :|  :: || |    ||| : |:|    ||:
Db        427 RIRASTGQAINSMEAGVSRVNEGVSFARQAGVSINEILDGTRHAASVVDEISQTIREQSR 486

Qy        442 STEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
              :::|:|: |: :  |: :   |: ::| ||    | : ||  |:
Db        487 ASDEIAQRVELIAQRSQQNTQAMHEMA-AT---ARRLNEVAATM 526
```

RESULT 2
US-10-389-647-531
; Sequence 531, Application US/10389647
; Publication No. US20040033549A1
; GENERAL INFORMATION:
; APPLICANT: GREENBERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candi
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: UIZ-038CP
; CURRENT APPLICATION NUMBER: US/10/389,647
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 531
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-531

Query Match 16.7%; Score 399.5; DB 4; Length 535;
Best Local Similarity 25.2%; Pred. No. 1.6e-15;
Matches 132; Conservative 111; Mismatches 206; Indels 75; Gaps 16;

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Qy          3 NDNDTLVTADVRNGIDGHALADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQPLFEATAD 62
              ::|:  | | :|| ::|  : |                :  | :||   ||   | |:
Db         37 SENELSVNA-LRNHMEGDMMHD---------------ALRADVLAAFVV-QPGDGAAAE 78

Qy         63 ALVTDFYDHLESYERTQDLFANSTKTVEQ-----LKETQAEYLLGLGRGEYDTEYAAQRA 117
               :  |  :| : :           | |||     | :   : |: | | : :    | :
Db         79 QVRQDLQEHSQWFR----------KVVEQNQGLPLNDAIHQALVEL-RPDLEAYIGAAES 127

Qy        118 RIGK-IHDVLGLGPDV--YLGAYTRYYTGLLDALADDV-----VADRGEE---------- 159
              :|| : | :    ::  :: |: :   |  :||:  :       :|  |
Db        128 IVGKALLDPVAARAELPQFVQAF-KELEGRNEALSSLIEKHVEQTNRAREDSMRYSAWML 186

Qy        160 ------AAAAVDELVARFL-----PMLKLLTFDQQIAMDTY-----IDS--YAQRLHDEI 201
                   |   : :|  : |     |: ||::  : ||         :||   | :|   :
Db        187 AGGILVACLVLGQLCRQLLRAVLQPLRKLVSSARVIAQGNLQEPIGVDSNDEAGQLQRAL 246

Qy        202 DSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASV 261
                ||    : | :      |  ||| : : : ::      | |    ::  :  :  ::
Db        247 GEMQENLRQMITIIRQESEELHDTSQSIGQTSQSIVHGASQQADSATSMAASMEEMITNI 306

Qy        262 EEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVE 321
              :::  ||: |  |  :| || |     : :  |: | :  :  :  :  ||: : ::
Db        307 SQISDHADNARVISAKSEELASSGGQVILNVVEGMSRIADVVNQSSTSITALGQSSDEIH 366

Qy        322 SVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVE 381
              |:  ||  ||||||:|||||:|||||||||| |||||||||: ||  : : :  : ::|
Db        367 SIIQVIKGIAEQTNLLALNAAIEAARAGEAGRGFAVVADEVRGLAARTTQSTQEITAMIE 426

Qy        382 QMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAV 441
              :::| | : :: ::    |: |||    :|  :: || |    ||| : |:|    ||:
Db        427 RIRASTGQAINSMEAGVSRVNEGVSFARQAGVSINEILDGTRHAASVVDEISQTIREQSR 486

Qy        442 STEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
              :::|:|: |: :  |: :   |: ::| ||    | : ||  |:
Db        487 ASDEIAQRVELIAQRSQQNTQAMHEMA-AT---ARRLNEVAATM 526
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RESULT 3
US-10-282-122A-66174
; Sequence 66174, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66174
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66174

Query Match 16.1%; Score 386.5; DB 4; Length 682;
Best Local Similarity 27.5%; Pred. No. 1.2e-14;
Matches 95; Conservative 77; Mismatches 140; Indels 33; Gaps 4;

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Qy        144 LLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDS 203
              ||| :||  :||     || | |                :  : |  ::  ||
Db        356 LLDEIAD--LADGDLTVAATVTE--------------------DFTGAIADSINYSIDQ 392

Qy        204 RQELA---NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSAS 260
               :||    |  |  | |     ::|:  :||        :: |   :|  |  |: :: |
Db        393 LRELVETINQTAVQVAAAAQETQSTAMHLAE-------ASEHQAQEIAGASAAINEMAVS 445

Qy        261 VEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADV 320
              :::|:: | :    :| : |:| :|     : :  | :| |     :  :::||| : ::
Db        446 IDQVSANASESSAVAERSVAIANKGNEVVHNTITGMDNIREQIQDTSKRIKRLGESSQEI 505

Qy        321 ESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELV 380
              :  :|:|||:|||:|||||:|:|: ||:|| |||||||||: ||| |   : ::| ||
Db        506 GDIVSLINDIADQTNILALNAAIQASMAGDAGRGFAVVADEVQRLAERSSAATKQIEALV 565

Qy        381 EQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQA 440
              : :| :| | |  :::    :  |    ::|   |:||    :  |: :| :| | :||
Db        566 KTIQTDTNEAVISMEQTTSEVVRGARLAQDAGVALEEIEKVSKTLAALIQNISNAARQQA 625

Qy        441 VSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
              |   ::  :: : :   : :|     | :     :   |:| :|
Db        626 SSAGHISNTMNVIQEITSQTSAGTTATARSIGNLAKMASEMRNSV 670
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RESULT 4
US-10-282-122A-69670
; Sequence 69670, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69670
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-10-282-122A-69670

Query Match 15.6%; Score 374.5; DB 4; Length 680;
Best Local Similarity 24.2%; Pred. No. 6.1e-14;
Matches 120; Conservative 103; Mismatches 201; Indels 71; Gaps 12;

```
Qy         23 ADRIGLDEAEIA----------WRLSFTGIDD-DTMAALAAEQPLFE---ATADALVTDF 68
              ||  | | ::              |  | ::| |  | ||    |||    : | ::
Db        207 ADAFGRDASQFGRVLNGMLEGNATLRITQVEDRDARARLAEIAELFEFVSGSVDEILETS 266

Qy         69 YDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHD-VLG 127
               :  :  | : ::| |:::|:          |  |           |  |:|  :  :   |||
Db        267 PELYQVREASGNIF-NTSQTLLDETSVLANSL----------ENLAKRRTMNTVGGYVLG 315

Qy        128 LGPDVYLGAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIA-- 185
              |      |   :    ||:      :| :   :      :       :::||   : :|
Db        316 L-----LALMSIILIGLV------MVRETNRQLRETAQKSERNQTAIMRLLDEIENLADG 364

Qy        186 --------MDTYIDSYAQRLHDEIDSRQELA---NAVATHVEAPLSSLEATSQDVAERTD 234
                     : :  : |  ::  ||  :||     |  |  | : ::  :||:  ::
Db        365 DLTVTASVTEDFTGAIADSINYSIDQLRELVVTINLTAEQVASAVTETQATAMQLS---- 420

Qy        235 TMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALA 294
                | :: |  :::  |  :: ::||:::|:: | :    :| : |:| :|     : :
Db        421 ---AASEHQALQISAASTAVNDMAASIDQVSANASESSAVAERSVAIANKGNEVVQNTIH 477

Qy        295 TMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEG 354
              | :| |      :  :::|||  : ::  :  :|||||:|||:|||||:|:|: ||:|| |
Db        478 GMDNIREQIQDTSKRIKRLGESSQEIGDIVSLIDDIADQTNILALNAAIQASMAGDAGRG 537

Qy        355 FAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMET 414
              ||||||||: ||| |   : ::| ||  :| :| | |  :::    :  |    ::|
Db        538 FAVVADEVQRLAERSSSATKQIETLVRAIQNDTNEAVISMEQTTSEVVRGARLAQDAGVA 597

Qy        415 LQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQ 474
              | ||        |  :: :: |  :|| |              ||:|:  :  |   | |
Db        598 LGEIEGVSRVLAELIESITDAAHQQAES-------------AGQISQTMTVIQQTTSQT 643

Qy        475 VRTVEEVRETVGKLS 489
                     |::| |:
Db        644 TSGTSATAESIGNLA 658
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RESULT 5
US-10-282-122A-68162
; Sequence 68162, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

```
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68162
;   LENGTH: 686
;   TYPE: PRT
;   ORGANISM: Pseudomonas putida
US-10-282-122A-68162

  Query Match             15.5%;  Score 371.5;  DB 4;  Length 686;
  Best Local Similarity   24.7%;  Pred. No. 9.2e-14;
  Matches  119;  Conservative   91;  Mismatches  196;  Indels   75;  Gaps   11;

Qy         37 LSFTGIDD-DTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLF--ANSTKTVEQLK 93
Db        237 IQVTRVEDADARARLAEIAELFQFVAGSVD-------EILETSPELFRVREAAGNIFSLS 289

Qy         94 ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDVV 153
Db        290 QTLLDEASHLANG-------FENLAGGRTLDTVG-----------GYVLGLL-ALASIIL 330

Qy        154 ----------------ADRGEEAAAAVDELVARFLPMLKLLTFDQQIA----------MD 187
Db        331 IGLVMVRTTNRQLRETAEKNERNQQAI----------MRLLDEIEELADGDLTVTVSVTE 380

Qy        188 TYIDSYAQRLHDEIDSRQELA---NAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQV 244
Db        381 DFTGAIADSINYSVDQLRDLVATINHSAVQVAAAVQDTQNTARQLAKASEHQAAQISEAS 440

Qy        245 DRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATD 304
Db        441 EAVGDMVESIDRVSAHAYESAKVA-------ERSVAIANKGNEVVHNTINGMDNIREQIQ 493

Qy        305 GVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKA 364
Db        494 DTAKRIKRLGESSQEIGDIVSLIDDIADQTNILALNAAIQASLAGEAGRGFAVVADEVQR 553

Qy        365 LAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVED 424
Db        554 LAERSSSATRQIEALVRTIQADTNEAVISMEQTTAEVVRGARLAQDAGVALAEIEGVSQN 613

Qy        425 AASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRET 484
Db        614 LADLIHSISDAAQLQTSSAGQISHTMAVIQQITAQTSAGSGATADSIRHLARMASEMRRS 673

Qy        485 V 485
              |
Db        674 V 674
```

```
RESULT 6
US-10-282-122A-77591
; Sequence 77591, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77591
;   LENGTH: 644
;   TYPE: PRT
;   ORGANISM: Vibrio cholerae
US-10-282-122A-77591

  Query Match             15.1%;  Score 361;  DB 4;  Length 644;
  Best Local Similarity   22.7%;  Pred. No. 3.5e-13;
  Matches  120;  Conservative   98;  Mismatches  212;  Indels   98;  Gaps   14;

Qy         28 LDEAEIAWRLSFTGIDDDTMAAL----AAEQPLF------------------------- 57
Db        139 LNQQQDGWFFGFIGSGKPTMVSMFQEANGEVKMFANYQLVNGNTMSGMSKSMDDMVRLLN 198

Qy         58 ----EATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLG-LGRGEYDTEY 112
Db        199 SFKIEDTGFVFLTNAQGEVQIHRQKEQV----KSSLQQIYGSGASALLNKSGFNLISTDY 254

Qy        113 AAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLL---DALAD-DVVADR---GEEAAAAVD 165
Db        255 QGEEVMVASI----------YIESMDWFLVGTVPVHEVFAELDAVAQRMMLTTLAVAAIF 304

Qy        166 ELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHD-----------EIDSRQELA----- 208
Db        305 IFMGIFLA--------NSIAMP--INQIAKRFTDLGRGDGDLSQRIEVKGNDEIAQLSKG 354

Qy        209 -NAVATHVEAPLSSLEATSQD-------VAERTDTMRARTDDQVDRMADVSREISSVSAS 260
```

```
Db        355 FNGFIEKIHQSIKDVAQTSRELQVAAEGVSRKALVTHDNSQQQRDQTIQVVTAINQMGAT 414

Qy        261 VEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADV 320

Db        415 ISEIASNAATAAETANQASGNADQGRNVVNKAKEAISRLAHDIENTGKVVEQLASTTQEI 474

Qy        321 ESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELV 380

Db        475 GSILDAIRGISEQTNLLALNAAIEAARAGDQGRGFAVVADEVRNLASRTASSTEEIQKMI 534

Qy        381 EQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQA 440

Db        535 NQLQNDAKNAVSAMDAGKTVTHQGVAASDEAVQVLMSISDRIHDISDRNTQVATATEEQS 594

Qy        441 VSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKL 488

Db        595 TVVHTINQNIEEINAINEVTTSTAEELADAS-------KSLRELSGRL 635


RESULT 7
US-09-272-809-5
; Sequence 5, Application US/09272809
; Patent No. US20020022239A1
; GENERAL INFORMATION:
;  APPLICANT: Lagarias, John C.
;  TITLE OF INVENTION: Phytofluors as fluorescent labels
;  FILE REFERENCE: 2500.118US0
;  CURRENT APPLICATION NUMBER: US/09/272,809
;  CURRENT FILING DATE: 1998-03-19
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 891
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:cph5 locus SLL0041
;   OTHER INFORMATION: (locus 1001300) an 891 aa protein,
;   OTHER INFORMATION: methyl-accepting chemotaxis protein I.  Homology
;   OTHER INFORMATION: to tsr in last 250 aa.
US-09-272-809-5

  Query Match             15.0%;  Score 359.5;  DB 3;  Length 891;
  Best Local Similarity   27.1%;  Pred. No. 6.3e-13;
  Matches  136;  Conservative   86;  Mismatches  197;  Indels   83;  Gaps   19;

Qy         23 ADRIGLDEAEIAWRLSFTGIDDDTMAALAAEQP--LFEATADALVTDFYDHLESY----- 75

Db        418 ADRV------IVYRFDATWAGTVIVESVAEGYPKALGATIADPCFADSY--VEKYRSGRI 469

Qy         76 ERTQDLFANSTKT---VEQLK--ETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGL-- 128

Db        470 QATRDIY-NAGLTPCHIGQLKPFEVKANLV----------------APINYKGNLLGLLI 512

Qy        129 -----GP------DVYLGAYTRYYTGLL----DALADDVVADRGEEAAAAVDELVARFLP 173

Db        513 AHQCSGPRDWHQNEIDLFGQLTVQVGLALERSDLLAQQKIAE--VEQRQMREKMQKRALE 570

Qy        174 MLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERT 233

Db        571 L--LMEVDPVSRGDLTIRAHV--TEDEIGTIADSYNATIESLRRIVTQVQTAASQFTETT 626

Qy        234 DT-------MRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGE 286

Db        627 DTNEVAVRQLAQQANRQALDVAEALERLQAMNKSIQAVAENAAQAESAVQRATQTVDQGE 686

Qy        287 AAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAA 346

Db        687 DAMNRTVDGIVAIRETVAATAKQVKRLGESSQKISKVVNLIGSFADQTNLLALNAAIEAA 746

Qy        347 RAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVE 406

Db        747 HAGEEGRGFAVVADEVRSLARQSAEATAEIAQLVATIQAETNEVVNAMEAGTEQVVVGTK 806

Qy        407 RVEEAMETLQEITDAVEDAASGMQE-VSTATDEQAVSTEE-------VAEMVD------- 451

Db        807 LVEETRRSLNQIT-AVSAQISGLVEAITSAAIEQSQTSESVTQTMALVAQIADKNSSEAS 865

Qy        452 GVDDRAGEIAAALDDIADATDQ 473

Db        866 GVSATFKELLAVAQSLQEAVKQ 887


RESULT 8
US-10-282-122A-51025
; Sequence 51025, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51025
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Bordetella pertussis
US-10-282-122A-51025

  Query Match             14.9%;  Score 356.5;  DB 4;  Length 539;
  Best Local Similarity   26.6%;  Pred. No. 5.3e-13;
  Matches  126;  Conservative   81;  Mismatches  153;  Indels  113;  Gaps   15;

Qy         38 SFTGIDDDTMAAL-----AAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQL 92

Db        126 SFAASLDEMMAALERNDDAAYLQLKNVKAGQASAAFAARLGEFSTNLDKLSSETLAAHET 185

Qy         93 KETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV 152

Db        186 RETIMLYV-----------YAA----------LLLLIVGVIAGSYLYMTRAVVRPLQR-- 222
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Qy        153 VADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVA 212
Db        223 -ASQQFERMAAGD-LSARI--------------------------EGNSRNEIGALLT 252

Qy        213 T--HVEAPLS-----------SLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSA 259
Db        253 ALRHMQESLTRTVAAVRRGVDEINVGSREISAGNTDLSSRTEEQ-------AASLEETAA 305

Qy        260 SVEEVAST----ADDVRRTSE---DAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQ 312
Db        306 SMEQLASTVKQNADNARQANQLAASASDVAESGGSAVSEVVSTM-------DGISASSRK 358

Qy        313 LGERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQ 372
Db        359 ISE-------IVSVIDGIAFQTNILALNAAVEAARAGEQGKGFAVVAGEVRSLAQRSAQA 411

Qy        373 STRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEV 432
Db        412 AKEIKVLIE----------DSVD----KVGTGSQQVERAGATMQEIVASVKRVTDIMGEI 457

Qy        433 STATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485
Db        458 SAASEEQSSGIEQVNRAVSQMDEVTQQNAALVEEAAAAAGSLQEQAQRLAEAV 510
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RESULT 9
US-10-389-647-372
; Sequence 372, Application US/10389647
; Publication No. US20040033549A1
; GENERAL INFORMATION:
; APPLICANT: GREENBERG, E. Peter
; APPLICANT: SCHUSTER, Martin
; APPLICANT: LOSTROH, Candi
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
; FILE REFERENCE: UIZ-038CP
; CURRENT APPLICATION NUMBER: US/10/389,647
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/653730
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/153022
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-372

Query Match 14.6%; Score 348.5; DB 4; Length 679;
Best Local Similarity 25.9%; Pred. No. 2.1e-12;
Matches 123; Conservative 78; Mismatches 179; Indels 95; Gaps 14;

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Qy         20 HALADRIGLDEAEI---AWRLSFTGIDDDTMAALAAEQPLFEATADAL--VTDFYDHLES 74
Db        242 HLLANLTGVHKAELNLGGRRFSLDVV-----------PVFNDANERLGSAVQWTDRTEE 289

Qy         75 YERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYL 134
Db        290 HRAEQE--------VSQLVQAAAA-----------GDFSKRVEEAGKEGFFLRLAKD--- 327

Qy        135 GAYTRYYTGLLDALADDVVADRGEEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYA 194
Db        328 ----------LNSLVD--TADRGLRD-------VSRMLGALAQGDLTQRIEAD-YQGTFG 367

Qy        195 QRLHDEIDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREI 254
Db        368 QLKDFSNDTAQSLSRMLGQIREA-ADTINTAASEIASGNAELSARTEQQASSLEETASSM 426

Qy        255 SSVSASVEEVASTADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLG 314
Db        427 EELTSTVKLNAENARQANSLAANASEVATQGGTVVQKVVSTMSSINES------------ 474
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Qy        315 ERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQST 374
Db        475 --ARKIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFAVVAGEVRTLAQRSAAAAK 532

Qy        375 RVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVST 434
Db        533 EIKTLIS----------DSVDKVE----NGNTLVAQAGQTMSDIVVAIRRVTDIMSEIAA 578

Qy        435 ATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKLS 489
Db        579 ASAEQSTGIEEVNSAVSQMDDMTQQNAALVEEAAAA-------AEAMQEQAGLLN 626
```

RESULT 10
US-10-282-122A-77066
; Sequence 77066, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77066
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77066

Query Match 14.5%; Score 348; DB 4; Length 626;
Best Local Similarity 27.4%; Pred. No. 2e-12;
Matches 92; Conservative 78; Mismatches 134; Indels 32; Gaps 6;

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Qy        174 MLKLLTFDQQI-----------AMDTYIDSYAQRLHDEIDSRQELANAVATHVEAPLSS 221
Db        298 MSPLKTLDSAIKDIASGGGDLTKKLDTNLDKEFSELALGFNSFTEMLGSQIRQLKTIASG 357

Qy        222 LEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEAL 281
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Db        358 VLDGAEKTANEAEVSRLVVEQQL-------QELEQLATAMNEMAMTASEVANSAQVAADA 410

Qy        282 AQQGEAAADDALATMTDIDEATDGVT-------AGVEQLGE--RAAD-VESVTGVIDDIA 331

Db        411 AKEGESA---SLEGSSVVHETTDAIQRLSIRIGSSVEDVKELVKATDRIETVLDVINDIA 467

Qy        332 EQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETV 391

Db        468 DQTNLLALNAAIEAARAGESGRGFAVVADEVRTLAQRTQQSTMQISEIIEQLQEGAKNVS 527

Qy        392 DQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVD 451

Db        528 RSMDESKLETDIVVEKTNQVNEKISLVQQAIHRISDMNLQIASAAEEQSLVAEEINNNTV 587

Qy        452 GVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGK 487

Db        588 NIKDLSIKLSEAASNAGTEMNAQVSKVKEQNELLNE 623


RESULT 11
US-10-282-122A-52305
; Sequence 52305, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52305
;   LENGTH: 686
;   TYPE: PRT
;   ORGANISM: Clostridium botulinum
US-10-282-122A-52305

  Query Match            14.1%;  Score 338;  DB 4;  Length 686;
  Best Local Similarity  26.8%;  Pred. No. 8.6e-12;
  Matches   91;  Conservative   80;  Mismatches  130;  Indels   38;  Gaps    4;

Qy        178 LTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAV-------ATHVEAPLSSLE---ATSQ 227

Db        350 LTEKVEIVNEDEIGKLSKIFNTMIDSLREITRNINNFSIQLAGSSQEILSSAEQTSAVSE 409

Qy        228 DVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSEDAEALAQQGEA 287

Db        410 EISSATEEIASGAENQVKASNESSLLMNDVMGNMYTLKEEFDEIISFSNNTNTLASKGQE 469

Qy        288 AADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNMLALNASIEAAR 347

Db        470 NMSNMVQQMATIKNSVVNSSNIMYDLQKNSEEIGNIVEIINTIADQTNLLALNASIEAAR 529

Qy        348 AGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEVNQRIGEGVER 407

Db        530 AGEAGKGFAVVADEVRKLAEESINSANNIKNLIMNTQDKTKTALNSIKDGASQSEKGESI 589

Qy        408 VEEAMETLQEI--------------------TDAVEDAASGMQEVSTATDEQAVSTEEV 446

Db        590 VAEVKESLGEILNSFSNVNHKFASVDSMITASNDSITAMASKLYDIETISNTASANTEEV 649

Qy        447 AEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETV 485

Db        650 AASTE-------EQSATIEEITESIEKLVSMVENLKESV 681


RESULT 12
US-10-332-288-28
; Sequence 28, Application US/10332288
; Publication No. US20040054165A1
; GENERAL INFORMATION:
;  APPLICANT: RAINEY, Paul Barton
;  APPLICANT:  SPIERS, Andrew Julien
;  APPLICANT:  BANTINAKI, Eleni
;  TITLE OF INVENTION: BACTERIAL POLYSACCHARIDE AND BIOFILM DEVELOPMENT
;  FILE REFERENCE: I0317.70012US00
;  CURRENT APPLICATION NUMBER: US/10/332,288
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: PCT/GB01/03077
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: UK 0016842.7
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Pseudomonas fluorescens
US-10-332-288-28

  Query Match            13.9%;  Score 332;  DB 4;  Length 547;
  Best Local Similarity  25.0%;  Pred. No. 1.5e-11;
  Matches  119;  Conservative   84;  Mismatches  189;  Indels   84;  Gaps   12;

Qy         66 TDFYDHLESYERTQDLFANSTKTVEQLKETQAEYLLGLGRGEYDTEYAA---------- 114

Db         89 TDKNDYKSFEARIEQQMANYEKTI----HGQAD------RMEFDNFKAAHINYNKVLAQV 138

Qy        115 -QRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDALADDV-VADRGEEAAAAVDELV---- 168

Db        139 LERVEANDLPGANQLLEEQLTPIWTEGRMKLNDIITENKNVSDR---ATAAIDEAVLSAK 195

Qy        169 ----------------------ARFLPMLKLLTFDQQIAMDTYID-SYAQRLH----DE 200

Db        196 ISMAVSLLIAILAAGLCGLLLMRAIMAPMQRIVDI-----LETMRDGDLSKRLNLERKDE 250

Qy        201 IDSRQELANAVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSAS 260

Db        251 FGAVETGFNDMMTELTALVSQAQRSSVQVTTSVTEIAATSKQQQATATETAATTTEIGAT 310

Qy        261 VEEVASTADDVRRTSEDAEALAQQGEAAA---DDALA----TMTDIDEATDGVTAGVEQL 313

Db        311 SREIAATSKDLVRTMTEVSTAADQASVAAGSGQQGLARMEETMHSVMGAADLVNAKLAIL 370
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Qy        314 GERAADVESVTGVIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQS 373
Db        371 NEKAGNINQVVVTIVKVADQTNLLSLNAAIEAEKAGEYGRGFAVVATEVRRLADQTAVAT 430

Qy        374 TRVEELVEQMQAETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVS 433
Db        431 YDIEQMVREIQSAVSAGVMGMDKFSEEVRRGMFEVQQVGEQLSQIIHQVQALAPRVLMVN 490

Qy        434 TATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGKLS 489
Db        491 EGMQAQATGAEQINH--------------ALVQLGDASSQTVESLRQASFAIDELS 532
```

RESULT 13
US-10-282-122A-77278
; Sequence 77278, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77278
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77278

Query Match 13.6%; Score 326; DB 4; Length 641;
Best Local Similarity 24.1%; Pred. No. 4e-11;
Matches 117; Conservative 97; Mismatches 164; Indels 108; Gaps 16;

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Qy         45 DTMAALAAEQPLFEATADALVTDFYDHLESYERTQDLFANSTKTVEQLKETQAE------ 98
Db        203 DTVRTLAEKAEKNAANIESLIKDISNGAE-------MVSNGVKSSSQKAESEVQKGHVVN 255

Qy         99 YLLGLGRGEYDTEYAAQRARIGKIHDVLGLGPDVYLGAYTRYYTGLLDAL-ADDVVADRG 157
Db        256 KQLTLIRNE----------MVDLVKD-----SEVLLKAADEMSSAAVIALKGSESVSQAA 300

Qy        158 EEAAAAVDELVARFLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELANAVATHVEA 217
Db        301 QEQSAACEE-------SLKSLD-QQQIALDGAVTA-AQSLDELTDELR------------ 339

Qy        218 PLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVASTADDVRRTSE- 276
Db        340 -------TSTDIVKSSEEVAAAAEELSAGIEEINRSSNEIMGALNQISSGAQHMAKSVET 392

Qy        277 ------DAEALAQQGEAAADDAL----------ATMTDIDE----ATDGVTAGVEQLGE 315
Db        393 GITSLTQIEQGARLGKERAESSLKACEKMLTGIEENKTTVDEMILAITESTKAATENLNE 452

Qy        316 RAADVESVTGVIDDIAE-------QTNMLALNASIEAARAGEAGEGFAVVADEVKALAEE 368
Db        453 -MANIERISRQIDKIVDGISNVSIQTAMLAVNGAVEAARAGEYGKGFAVVSTDIQNLAND 511

Qy        369 SREQSTRVEELVEQMQAE--------------TEE------TVDQLDEVNQRIGEGVER 407
Db        512 AAENAEQIKDQVKNIQEQINIVRKDLADILSTVMEEAQKAALTIKQLDNVRSRMSDVVLG 571

Qy        408 VEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRAGEIAAALDDI 467
Db        572 SKRISESAGGIERSIADARAGMQQIATAAEESSHATGEAATAARQQSSSTSELASAIENI 631

Qy        468 ADATDQ 473
Db        632 AAVADE 637
```

RESULT 14
US-10-282-122A-77602
; Sequence 77602, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

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;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77602
;   LENGTH: 643
;   TYPE: PRT
;   ORGANISM: Vibrio cholerae
US-10-282-122A-77602

  Query Match             13.2%;  Score 315;  DB 4;  Length 643;
  Best Local Similarity   24.9%;  Pred. No. 1.8e-10;
  Matches  100;  Conservative   77;  Mismatches  167;  Indels   58;  Gaps   10;

Qy        133 YLG-AYTRYYTGLLDALADD------VVADRGEEAAAAVDELVAR---------------- 170
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Db        249 YLGIEFDGYYKRV--NLTDDMYWTLMVFVDKA-TALADVDVAVANAITTGIVLIGISVGV 305

Qy        171 --------FLPMLKLLTFDQQIAMDTYIDSYAQRLHDEIDSRQELAN------------- 209
                      : |:|:|      :|  :      :|| |::   :||
Db        306 IIFIINQIYKPLLRLKVAVLDLAQGS--GDLTRRL--EVNGNDDLAQISEGFNRFSGNLQ 361

Qy        210 ----AVATHVEAPLSSLEATSQDVAERTDTMRARTDDQVDRMADVSREISSVSASVEEVA 265
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Db        362 NMMLQISDATQIISSSIEQLSQ-TAKENEQMLISHSSETDQ---VVTAITQMSESARTVA 417

Qy        266 STADDVRRTSEDAEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTG 325
               :    : :| |   |||      ::|::|:| :    : ::  :  :   |  : |
Db        418 ESVTQSNQITEAASKEAQQSLVIVNNAVSTVTSLVNDVENMSESISNMNRDANKISEVLS 477

Qy        326 VIDDIAEQTNMLALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQA 385
              ||  |:||||:|||||:|||||||| | |||||||||:|||  ::  :| : ::: ::
Db        478 VIGAISEQTNLLALNAAIEAARAGEQGRGFAVVADEVRALAARTQNSTTEISDMLTKLLE 537

Qy        386 ETEETVDQLDEVNQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEE 445
               |:  |  ::   |:       ::  |  :|  :: :| |       ::: ||::|:    |
Db        538 GTDSVVGAMERTKQQCQTTADKTSEVSGSLNMMSASVSDIDDLSTQIAAATEQQSTVAAE 597

Qy        446 VAEMVDGVDDRAGEIAAALDDIADATDQQVRTVEEVRETVGK 487
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RESULT 15
US-10-282-122A-69564
; Sequence 69564, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69564
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Pseudomonas syringae
US-10-282-122A-69564

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Qy        176 KLLTFDQQIAMDTYID-------SYAQRLHDEIDSRQELANAVATHVEAPLSSLEATSQD 228
              ::|    | : |: ||       | |||    :     | : |           |      |
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Qy        229 VAERTDTMR----------ARTDDQVDRMADVSREISS-VSASVEEVASTADDVRRTSED 277
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Db        240 LAKASGTLETGAQHQLSEIARMTGAMQRMGDAMNDISGHVAQAVQRAGDASDQV------ 293

Qy        278 AEALAQQGEAAADDALATMTDIDEATDGVTAGVEQLGERAADVESVTGVIDDIAEQTNML 337
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Db        294 -----AHGRDSVDRAQSEITQLAARISTTDETVQALANQSEQIGKVLDVIGSIAEQTNLL 348

Qy        338 ALNASIEAARAGEAGEGFAVVADEVKALAEESREQSTRVEELVEQMQAETEETVDQLDEV 397
              ||||:||||||| | |||||||||: ||: :   :  :: ::| :|  : :     : :
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Qy        398 NQRIGEGVERVEEAMETLQEITDAVEDAASGMQEVSTATDEQAVSTEEVAEMVDGVDDRA 457
               | :|  ||  : | |:|: : : :         ::| |::|| :: |:|: :  |   |
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Qy        458 GEIAAALDDIADAT 471
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